

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 25, 2005, 20:19:56 ; Search time 75 Seconds
(without alignments)
301.479 Million cell updates/sec

Title: US-09-874-140-2
Perfect score: 1206
Sequence: 1 MTQPASSRVFDPSPNPTTFS.....KGQTLSHGTQSGNASRRV 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	235	1 WZBE23	gene 23 protein -
2	154.5	12.8	119	2 T42568	probable capsid pr
3	153.5	12.7	119	1 WZBE27	13.6K capsid prote
4	139	11.5	710	1 QZBE22	membrane antigen g
5	131.5	10.9	2232	2 T34434	hypothetical prote
6	128	10.6	310	1 PIHUSD	salivary proline-r
7	128	10.6	1151	2 T18535	high molecular mas
8	127	10.5	721	2 E70766	hypothetical prote
9	127	10.5	780	2 T00366	hypothetical prote
10	126	10.4	775	2 I43759	hepatocyte growth
11	125	10.4	1357	2 T29265	hypothetical prote
12	124.5	10.3	907	1 QZBE21	membrane antigen g
13	124.5	10.3	1032	2 T34433	hypothetical prote
14	123	10.2	392	1 PIHUB6	salivary proline-r
15	122.5	10.2	886	2 S29605	glycoprotein 350/2
16	122.5	10.2	1275	2 T33369	hypothetical prote
17	122	10.1	1096	1 S61917	protein kinase C (
18	122	10.1	1199	2 A40670	nuclear envelope p
19	122	10.1	2441	2 S39161	CREB-binding prote
20	121.5	10.1	3164	1 WMBEH6	UL36 protein - hum
21	121	10.0	251	1 PIHUPF	salivary proline-r
22	121	10.0	678	2 JC4245	transcription fact
23	119.5	9.9	604	2 A39369	homeotic protein B
24	119	9.9	1415	1 EDBEGA	immediate-early pr
25	118.5	9.8	542	2 S64030	probable membrane
26	118	9.8	319	2 T11592	hypothetical prote
27	118	9.8	333	2 S11484	CABP1 protein - sl
28	117.5	9.7	220	2 A36298	proline-rich prote
29	117.5	9.7	1794	2 T38459	hypothetical diver

30	117	9.7	606	2 S13367	Om(1D) protein - f
31	117	9.7	1952	2 T48814	hypothetical prote
32	117	9.7	2440	2 S39162	transcription coac
33	116.5	9.7	677	2 T00369	hypothetical prote
34	115.5	9.6	419	2 T04530	hypothetical prote
35	115.5	9.6	419	2 D85334	hypothetical prote
36	115.5	9.6	838	1 ESWTHW	glutenin, high mol
37	115.5	9.6	1390	2 T31353	polyprotein - Arab
38	115.5	9.6	3942	2 T42730	Basoon protein -
39	115	9.5	666	2 B70803	hypothetical prote
40	114.5	9.5	212	2 B36298	proline-rich prote
41	114.5	9.5	324	2 S13497	CAMP-binding prote
42	114.5	9.5	510	2 H84824	En/Spm-like transp
43	114.5	9.5	539	2 T28770	hypothetical prote
44	114.5	9.5	587	2 T41653	probable transcrip
45	113.5	9.4	309	2 S10889	proline-rich prote

ALIGNMENTS

RESULT 1

WZBE23
gene 23 protein - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: E27343
R:Davidson, A.J.; Scott, J.E.
J: Gen. Virol. 67, 1759-1816, 1986
A:Title: The complete DNA sequence of varicella-zoster virus.
A:Reference number: A27345; MUID:86306657; PMID:3018124
A:Accession: E27343
A:Molecule type: DNA
A:Residues: 1-235 <DAV>
A:Cross-references: UNIPROT:P09279; EMBL:X04370; NID:959989; PIDN:CAA27906.1; PID:960012
C:Genetics:
A:Gene: 23

Query Match	100.0%	Score	1206;	DB	1;	Length	235;
Best Local Similarity	100.0%	Pred. No.	2.7e-69;				
Matches	235;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MTQPASSRVFDPSPNPTTFSVEAIAAAYTPVALIRLLNASGPIQGHVRVDIADARSITYTVG	60				
Db	1	MTQPASSRVFDPSPNPTTFSVEAIAAAYTPVALIRLLNASGPIQGHVRVDIADARSITYTVG	60				
QY	61	AAASARARAHNANTIRRTAMFAETDPMWLRTVGLKRTFNPRIRPQPNPMSLGI	120				
Db	61	AAASARARAHNANTIRRTAMFAETDPMWLRTVGLKRTFNPRIRPQPNPMSLGI	120				
QY	121	SGPTLPKQTSADQSALQQPAALAFSGSSQHPHPPQTTSASVGGQHQHVSSGQQPOQ	180				
Db	121	SGPTLPKQTSADQSALQQPAALAFSGSSQHPHPPQTTSASVGGQHQHVSSGQQPOQ	180				
QY	181	GAQSSTVQPTTGPSPAAQGVFPQSTPPPTQNTPPQGGKGTLSHTGSGNASRRV	235				
Db	181	GAQSSTVQPTTGPSPAAQGVFPQSTPPPTQNTPPQGGKGTLSHTGSGNASRRV	235				

RESULT 2

T42568
probable capsid protein 25 - equine herpesvirus 4 (strain NS80567)
C:Species: equine herpesvirus 4
A:Variety: strain NS80567
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42568
R:Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davidson, A.J.
J: Gen. Virol. 79, 1197-1203, 1998
A:Title: The DNA sequence of equine herpesvirus-4.
A:Reference number: Z22173; MUID:98264497; PMID:9603335
A:Accession: T42568

A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-119 <TEL>
A:Cross-references: UNIPROT:O39267; EMBL:AF030027; NID:G2605950; PIDN:AAC59540.1; PID:g2605950
A:Experimental source: strain NS80567
C:Genetics: 25
A:Note: 25
C:Superfamily: human herpesvirus 1 UL35 protein; human herpesvirus 1 UL35 protein homolog

Query Match 12.8%; Score 154.5; DB 2; Length 119;
Best Local Similarity 32.8%; Pred. No. 0.0019;
Matches 38; Conservative 12; Mismatches 39; Indels 27; Gaps 3;

QY 9 VVFDPSNPTTFSVEALAAATPVALIRLLNASGLPQGHVRVDIADARSIIYT-----58
Db 12 VAFDPWDPTNKAANFKDMLPVDVMTILN-----QNIDELD-----YTKYSDDEINSG 59

QY 59 -----VGAASAARARANHNANTIRRTAMPAETDPTMTWLRPTVGLKRTFNRIIRP 109
Db 60 LKQLEFMGTAKTWVLRQRHLKALVRSFAHNDASTWARPNIGLKRTFPFRFMQP 115

RESULT 3
WZBEB7
13.6K capsid protein - equine herpesvirus 1 (strain Ab4p)
C:Species: equine herpesvirus 1
A:Note: host Equus caballus (domestic horse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: H36797
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
A:Description: The DNA sequence of equine herpesvirus-1.
A:Reference number: A36805
A:Accession: H36797
A:Molecule type: DNA
A:Residues: 1-119 <TEL>
A:Cross-references: UNIPROT:P28974; GB:M86664; NID:G330791; PIDN:AAB02460.1; PID:G330817
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virolgy 189, 304-316, 1992
A:Title: The DNA sequence of equine herpesvirus-1.
A:Reference number: A41831; MUID:92295566; PMID:1318606
A:Contents: annotation; possible protein-coding frames
A:Note: neither amino acid nor nucleotide sequence is given
C:Genetics:
A:Gene: 25
C:Superfamily: human herpesvirus 1 UL35 protein; human herpesvirus 1 UL35 protein homolog
C:Keywords: capsid protein
F;19-110/Domain: human herpesvirus 1 UL35 protein homology <UL35>

Query Match 12.7%; Score 153.5; DB 1; Length 119;
Best Local Similarity 31.1%; Pred. No. 0.0022;
Matches 37; Conservative 16; Mismatches 45; Indels 21; Gaps 3;

QY 3 QPASSRVFDPSNPTTFSVEALAAATPVALIRLLNASGLPQGHVRVDIADARSIIYT-----58
Db 6 QQQQAPVAEPADPNPKAANFKDMLPVDVMTILN-----QNIDELDYTK-YTEDEI 56

QY 59 -----VGAASAARARANHNANTIRRTAMPAETDPTMTWLRPTVGLKRTFNRIIRP 109
Db 57 SEGKQLFMGTAKTWVLSLRHLKSLVRRSDMFQNDASTWARPNIGLKRTFPFRFMQP 115

RESULT 4
QOBE22
membrane antigen gp220 - human herpesvirus 4 (strain B95-8)
C:Species: human herpesvirus 4, Epstein-Barr virus
C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C:Accession: B43042; A03763
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A:Reference number: A93065; MUID:85035713; PMID:6092825
A:Accession: B43042

A:Molecule type: DNA
A:Residues: 1-710 <BAN>
A:Cross-references: UNIPROT:P03200
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; Ha
Nature 310, 207-211, 1984
A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A:Reference number: A03794; MUID:84270667; PMID:6087149
A:Contents: annotation; protein coding region
C:Superfamily: Epstein-Barr virus membrane antigen gp220

Query Match 11.5%; Score 139; DB 1; Length 710;
Best Local Similarity 25.5%; Pred. No. 0.11;
Matches 56; Conservative 25; Mismatches 101; Indels 38; Gaps 9;

QY 37 NASGLPQGHVRVDIADARSIIYTVGAAGAAR-----ARANHNANTIRRTAMPAETDPTMTWL 92
Db 378 NISGAFASNRITDI-----TVSLGTAPKTLIIRATNATTTTHKVIKAPESITTT 430

QY 93 RPTVGLKRTFNRIIRPQPPNPSMLGISGPTLPKQTSADOSALQOAPALAFSGSSSQ 152
Db 431 SPTLNTTGFADPNTTTGLPSSHTVPTNLTPASTGPTVSTADVTS-PTPAGTT-SGASPV 488

QY 153 HPPP-----QTTASVGVQOOHVVGSSGQPOQOQASSTVQP---TTGSP 195
Db 489 TPSPSPWDNGTESGENITQVTPASI--STHVSTSS-PAPRPGTTTSQASGPGNSSTSTKP 545

QY 196 AAQGVQPOSTPPTQNTPOGKGQ-----TLSHTGSGNAS 230
Db 546 GRVNTKGTTPQNAVSPQAPSGQKTAVTPTVSTGKANST 585

RESULT 5
T34434
hypothetical protein K06A9_1a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34434
R;Geisel, C.; Gattung, S.
A:Description: The sequence of C. elegans cosmid K06A9.
A:Reference number: Z21525
A:Accession: T34434
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2232 <GEI>
A:Cross-references: UNIPROT:O81PX6; EMBL:U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:K06A9
A:Experimental source: strain Bristol N2; clone K06A9
C:Genetics:
A:Gene: CESP:K06A9.1a
A:Map position: X
A:Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 2075/1;

Query Match 10.9%; Score 131.5; DB 2; Length 2232;
Best Local Similarity 26.0%; Pred. No. 1.1;
Matches 69; Conservative 29; Mismatches 130; Indels 37; Gaps 10;

QY 2 TQPASSRVVFDPSNPTTFSVEALAAATPVALIRLLNASGLPQGHVRVDIADARSIIYTVG 60
Db 859 TSSGSGSMITQSPYPSQSTSPVESSTTPSPGSGTTLTSTSP-SPSQSTTIGTQGSTSPG 917

QY 61 AAASAARARANHNANTIRRTAMPAETDPTMT-----WLRPTVG-LKRTFNRIIRPQPP 112
Db 918 ISTTSEMTSQSTQTPGSGS-TVTPSTVSDSTSSGSGTPTVVGSTEGSSPTPSTQNT 976

QY 113 NPSMSLIGISGPTLPKQTSADOSALQOAPALAFSGS-----SPQHPPTQTTASVGS 164
Db 977 NPSTSGSGSMSTQTPQSSQSTSPVESSTSGATSSSGSGSGTTLTSTSPSPSPSTTSSSQ 1036

QY 165 QQQHVVGSG-SSGQQPQOQGAQSSTV-QPTTGSPPAAQGV-----POSTPPP 207
Db 1037 STSPVVTISQGSTETPGTGTGTVPKSTVSGSASSGATATMGSTASSTSGSSSTSPN 1096

QY 208 TQNTPGGKGQTLTSHTGSGGNASRS 232

A;Introns: 22/1; 34/1
A;Note: the list of introns may be incomplete
C;Superfamily: proline-rich protein
C;Keywords: glycoprotein; saliva; tandem repeat
F;1-16/Domains: signal sequence #status predicted <SIG>
F;241-310/Product: proline-rich peptide p-D #status experimental <MAT>
F;66,87,171/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;108,150,192,213,234/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.6%; Score 128; DB 1; Length 310;
Best Local Similarity 25.7%; Pred. No. 0.23;
Matches 56; Conservative 16; Mismatches 99; Indels 48; Gaps 8;

QY 30 VALIRLLNAGPLQCHRVDIADARSIVTVGAASAARARAHNHANTTTRTAMFAETDPM 89
||| : : : ||| : : :
Db 8 VALLALSSAESSE-----DVQEESLFLISGKQRRPQGNGPOQ----- 48

QY 90 TWLRPTVGLKRTFNRIIRPPNPMSLSIGISGTPILPKQTQSADQSALQQPAALAFSGS 149
||| : : : ||| : : :
Db 49 ----RPP-----PPPGKQPDPGGNQSQGPPPPGKPEGRPPQCGNQSQGPPPHGP 97

QY 150 SPQHPPPTTSASVGQQHVVSGSGGQOPQCAQSSTVTQTTGSP--PAAQGVQPS--TP 205
||| : : : ||| : : :
Db 98 KPERPPPGGNQSQGPPPHGKPES-RPPQGHQSQGPPPTPKPEGPPQCGNQSQGTTP 156

QY 206 P----PTQNTPOGGK-----GQTLSHTGQSGNAS 230
||| : : : ||| : : :
Db 157 PPPGKPEGRPPQCGNQSQGPPPHGKGERPPPPQCGNQGS 194

RESULT 7
T18535
high molecular mass nuclear antigen - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18535
R;Shimada, K.; Harata, M.; Mizuno, S.
J. Cell Sci. 110, 3031-3041, 1997
A;Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, of
A;Reference number: Z18955; MUID:9803440; PMID:9365273
A;Accession: T18535
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1151 <SHI>
A;Cross-references: UNIPROT:O57580; EMBL:D88440; NID:d1177138; PID:d1025045; FIDN:B

Query Match 10.6%; Score 128; DB 2; Length 1151;
Best Local Similarity 28.2%; Pred. No. 0.92;
Matches 57; Conservative 22; Mismatches 81; Indels 42; Gaps 11;

QY 59 VGAA-----ASAAARAHNHANTTIRRTAMFAETDPTWLRLPTVGLKRTFNPRIIR 109
||| : : : ||| : : :
Db 776 MGAAATTPQSPMGAAATQVATSAGNTWQVSPMGATPPQT---PSVGAATT-----P 825

QY 110 QPNPMSLSIGISGTPILPKQTQSADQSAL-QQPAALAFSGSSPHQP-----PQT--SA 161
||| : : : ||| : : :
Db 826 QPSPMGAAATTLSPMGAAATTPQSPMGAVTTQPPMAATNTT-QPPPMAASTPQSTPMGA 884

QY 162 SVGQQHVVSGSGGQOPQCAQSSTVQDT-TGSP-----PAAQGVQPS--STPPT 208
||| : : : ||| : : :
Db 885 ATTTQSPPMGAVTTQSPPMGASTPQAAPTVAAGSPTPPPIPPSPAQTSQPMKSPPPD 944

QY 209 QNTPOGGKGQTLSHTGQSGNAS 230
||| : : : ||| : : :
Db 945 PPKAPSAAAQT-SPAHHVANAS 965

RESULT 8
E70766
hypothetical protein Rv2082 - Mycobacterium tuberculosis (strain H37Rv)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: E70766

Db 649 AVTTGQHNITSSSTSSMLRSPSSNPETLSPSTSDNSTSHMPLLTSAHPTGGENITQVTPA 708
Qy 162 SVGQQQHVSVSSGQQPQQGAGSSTVQP---TTGSPPPAAQGVPPQSPPTPTTQNTPOGKGQ 218
Db 709 SI--STHHVSTSS-PAPRPGITTSQASGPGNSSTSTKPGENVVTKGTPPQNATSPQAPSGQ 765
Qy 219 -----TSLSHTCQSGNAS 230
Db 766 KTAVPTVTSTGGKANST 782

RESULT 13
T34433
hypothetical protein K06A9.1a - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T34433
R/Geisel, C.; Gattung, S.
submitted to the EMBL Data Library, December 1996
A/Description: The sequence of C. elegans cosmid K06A9.
A/Reference number: Z21525
A/Accession: T34433
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1032 <GEI>
A/Cross-references: UNIPROT:P91365; EMBL:U80846; PIDN:AAC70889.1; GSPDB:GN00028; CESP:K06A9
A/Experimental source: strain Bristol N2; clone K06A9
C/Genetics:
A/Map position: X
A/Genes: CESP:K06A9.1a
A/Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 839/1; 849/1; 875/3; 940/2; 966/2; 993/2

Query Match 10.3%; Score 124.5; DB 2; Length 1032;
Best Local Similarity 23.3%; Pred. NO. 1.4;
Matches 59; Conservative 33; Mismatches 108; Indels 53; Gaps 11;

Qy 7 SRVVFDSNPPTFSVEATAATPVALLRNASGFLPGHRVYDIADARSITYTVGAAASAA 66
Db 419 STTVAVPSSSTF-----GSSTPIA-----SSSSGSTVTVVSGSS-STVGSSTPSA 464
Qy 67 RARANHANTIRRTAMFAETDPTWLRVTGLKRTFNPRRIIRPQPPNPSMLGISGP--- 123
Db 465 SSSSAGTASTIS-----GSTGSTATVP--GSSSSVSGSSTQSASPSPTMTSVSGPTGS 517
Qy 124 --TILPKQTQAGDSALQOPAA-----LAFSGSP---QHPPPTTSASVCGQQHV 170
Db 518 TTVTVPGSSTPAPSSSPNPSSPASTGSTITIGSSSIIIVSVSGSTVSGSTGTSGSTL 577
Qy 171 SGS-----SGQPQPGAGSSTVQPTTGPSPAAQGVQSTPP---PTQNTPOGGK 216
Db 578 ASSTATPGSSSTVPSSSSPQSSQSPA--PNTGSTTPTSGTSSQSPSPMNPSSSTPTGSS 635
Qy 217 GQTLSHTCQSGNA 229
Db 636 QSTTPEGSTASS 648

RESULT 14
PIHUB6
salivary proline-rich phosphoprotein precursor PRB1 (large allele) [validated] - human
N/Contains: peptide IB-1; peptide P-E (peptide IB-9); peptide P-F; peptide P-H
C/Species: Homo sapiens (man)
C/Date: 04-Dec-1986 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C/Accession: B40750; A40750; C25372; S02128; S02127; A03293; A90502; A91974; A051
R/Azen, E.A.; Latreille, P.; Niece, R.L.
Am. J. Hum. Genet. 53, 264-278, 1993
A/Title: PRB1 gene variants coding for length and null polymorphisms among human salivary
A/Reference number: A40750; MUID:93304421; PMID:8317492
A/Accession: B40750
A/Molecule type: DNA
A/Residues: 35-392 <AZE>
A/Cross-references: UNIPROT:P04280; UNIPROT:P04281; UNIPROT:P02811; UNIPROT:Q16038; GB:S

A;Experimental source: subject C.J. (large allele)
A;Accession: C40750
A:Molecule type: DNA
A;Residues: 35-127,'R',129-148,'R',150-151,153-187,'K',189-272,'S',274-336,'S',338-392 <A23>
A;Cross-references: GB:S62929
A;Experimental source: subject M.V.O. (large allele)
A;Accession: A40750
A:Molecule type: DNA
A;Residues: 35-183,245-270,'O',272-392 <A23>
A;Cross-references: GB:S62928
A;Experimental source: subject C.J. (medium allele)
A;Note: authors translated the codon CAA for residue 272 as Arg
R;Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O.
J. Biol. Chem. 260, 11123-11130, 1985
A;Title: Differential RNA splicing and post-translational cleavages in the human salivary gland
A;Reference number: A92492; MUID:85289325; PMID:2993301
A;Accession: C25372
A:Molecule type: mRNA
A;Residues: 1-183,245-392 <MAE>
A;Cross-references: GB:K03204; NID:gi90485; PIDN:AAAG0185.1; PID:gi90486
A;Note: alternatively splice forms lacking portions of the repeat region were also found
R;Lyons, K.M.; Stein, J.H.; Smithies, O.
Genetics 120, 267-278, 1988
A;Title: Length polymorphisms in human proline-rich protein genes generated by intragenic recombination
A;Reference number: S02127; MUID:89121440; PMID:2851479
A;Accession: S02128
A;Status: translation not shown
A:Molecule type: DNA
A;Residues: 35-127,250-273,'R',275-277,'R',279-336,'S',338-392 <LYO>
A;Cross-references: EMBL:X07517
A;Accession: S02127
A;Status: translation not shown
A:Molecule type: DNA
A;Residues: 35-183,245-392 <LY2>
A;Cross-references: EMBL:X07516
R;Kaufman, D.; Hofmann, T.; Bernick, A.; Keller, P.
Biochemistry 25, 2387-2392, 1986
A;Title: Basic proline-rich proteins from human parotid saliva: complete covalent structure
A;Reference number: A90502; MUID:86243355; PMID:3521730
A;Accession: A03293
A:Molecule type: protein
A;Residues: 17-38,'AP',41-51,92-148,'R',150-152 <KA2>
A;Note: among nine basic proline-rich peptides isolated from the saliva, this peptide is the most abundant
A;Accession: A90502
A:Molecule type: protein
A;Residues: 275-336,'S',338-392 <KAU>
R;Saitoh, E.; Isemura, S.; Sanada, K.
J. Biochem. 94, 1991-1999, 1983
A;Title: Further fractionation of basic proline-rich peptides from human parotid saliva
A;Reference number: A91974; MUID:84161824; PMID:6671974
A;Contents: P-H
A;Accession: A91974
A:Molecule type: protein
A;Residues: 'S',338-392 <SAI>
R;Azen, E.; Lyons, K.M.; McGonigal, T.; Barrett, N.L.; Clements, L.S.; Maeda, N.; Vanin, J.
Proc. Natl. Acad. Sci. U.S.A. 81, 5561-5565, 1984
A;Reference number: A94005; MUID:84298176; PMID:6089212
A;Accession: A05261
A:Molecule type: DNA
A;Residues: 35-39,'P',41-84,'G',86,'R',87-154,'R',218-246;300-306,'T',308-329,'C',331-382 <A25>
A;Accession: A05262
A:Molecule type: DNA
A;Residues: 'N',57-59,'A',61-69;334-336,'S',338-339,'R',341-392 <A25>
R;Kaufman, D.; Wong, R.; Bernick, A.; Keller, P.
Biochemistry 21, 6558-6562, 1982
A;Title: Basic proline-rich proteins from human parotid saliva: complete covalent structure
A;Reference number: A90464; MUID:83101329; PMID:6924859
A;Contents: IB-9
A;Accession: A90464
A:Molecule type: protein
A;Residues: 92-127,'R',129-148,'R',150-152 <KA3>
R;Isemura, S.; Saitoh, E.; Sanada, K.
J. Biochem. 91, 2067-2075, 1982

A;Title: Fractionation and characterization of basic proline-rich peptides of human parotid gland
A;Reference number: A91966; MUID:83007119; PMID:7118863
A;Contents: P-E
A;Accession: A91966
A:Molecule type: protein
A;Residues: 92-127,'R',129-148,'R',150-152 <ISE>
C;Comment: This peptide contains 21-residue repeats, two of which have internal 7-residue repeats
C;Genetics:
A;Gene: GDB:PRB1
A;Cross-references: GDB:119511; OMIM:180989
A;Map position: 12p13.2-12p13.2
A;Note: each of the tandem repeats contains a candidate splice acceptor site, and several repeats are interrupted by a stop codon
C;Superfamily: proline-rich protein
C;Keywords: alternative splicing; duplication; parotid gland; phosphoprotein; pyroglutamin
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-51,92-152/Product: basic proline-rich peptide IB-1 #status experimental <IB1>
F;52-152/Product: basic proline-rich peptide P-E #status experimental <PE>
F;275-392/Product: basic proline-rich peptide IB-6 #status experimental <PIB6>
F;275-335/Product: basic proline-rich peptide P-F #status experimental <PPF>
F;337-392/Product: basic proline-rich peptide P-H #status experimental <PPH>
F;17/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F;24/Binding site: phosphate (Ser) (covalent) #status experimental
Query Match 10.2%; Score 123; DB 1; Length 392;
Best Local Similarity 32.4%; Pred. No. 0.62;
Matches 44; Conservative 7; Mismatches 59; Indels 26; Gaps 6;
QY 108 RPQPNPMSLIGSGFTILPKQTQSADQSALQQAALAFSGSSPOHPPPQ-----TTSAS 162
DB 218 KPQGPFPQGGNQPPPPPPPPGKPPQGGNNRPPPG-KPQGPFPQGGKSRSPQSP 276
QY 163 VQOQOHVWSGSGQQPQQAQSSVTQPTTGSPPAAQGVFPQSTPPPTTQNTFQG----GKQ 218
DB 277 PKPQ-----GPPPPQGGNQPP-----GPPPPGKPPQGGNKPQGGPPPGKPK 322
QY 219 TLSHTGQSGNRSRR 234
DB 323 --GPPAQGGKSGQSAR 336
RESULT 15
S29605
glycoprotein 350/220 - human herpesvirus 4
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S29605
R;Klein, K.; Mueller-Lantzsch, N.
submitted to the EMBL Data Library, October 1992
A;Description: Sequences of the membrane proteins gp 350/220 and p140 of Epstein-Barr virus
A;Reference number: S29605
A;Accession: S29605
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-886 <KLE>
A;Cross-references: UNIPROT:Q07284; EMBL:X67776; NID:g59163; PIDN:CAA47986.1; PID:g59164
C;Superfamily: Epstein-Barr virus membrane antigen gp350
C;Keywords: glycoprotein
Query Match 10.2%; Score 122.5; DB 2; Length 886;
Best Local Similarity 22.4%; Pred. No. 1.6;
Matches 56; Conservative 33; Mismatches 110; Indels 51; Gaps 8;
QY 2 TOPASSRVVDFSNPTTFSVEIAAYTPVALIRLLNASGLQPGHRVDIADARSIVTGA 61
DB 542 TSPTSA-VTTTPNATSTPAVTPFPNATPTLTKTSP----- 579
QY 62 AASAFARAHNANTIRRTAMFAETDPMTWLRTVGLKFTFNPRIRIRPFPNPSMSLGIS 121
DB 580 TSAVTTPTENATSPVTGETSPQANTTNHT-----LGGTSSPTVVTSPPKNATSAVTG 632
QY 122 GTTILPKQTQSAD--QSALQQAALAFSGSSPQHPPPTTSASVGOQ-----H 168
DB 633 QHNITSSSTSSMSLRPSSISETLSPTSDNSTSHMPLLTSAHPTGGENITQVTPASTSTH 692

Qy 169 VVSGSGQOQOQAGSSTVQP---TTGSPPAAGVVPQSTPTPTQNTPOGKGQ-----TL 220
Db 693 HVSTSS-PAPRPGTTTQASGPGNSSTTKPGEVNTKGTTPKNATSPQAPSGQKTAVPTV 751
Qy 221 SHTGOSGNAS 230
Db 752 TSTGGKANST 761

Search completed: September 25, 2005, 21:03:20
Job time : 76 secs

Large blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 25, 2005, 15:48:09 ; Search time 326 Seconds
(without alignments)
278.800 Million cell updates/sec

Title: US-09-874-140-2

Perfect score: 1206

Sequence: 1 MIQPASRVVDPNSPTTFS.....KGQTLSTGQGNASRRRV 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	235	2	AAY25337 VZV VP26
2	146	12.1	1367	7	ADB70311 C. neofor
3	133.5	11.1	496	8	ADR08679 Human pro
4	127.5	10.6	907	1	AAP50073 Epstein-B
5	127.5	10.6	907	2	ABR80144 EBV gp350
6	127.5	10.6	907	3	AAY68009 Epstein-B
7	127	10.5	634	8	ABO84900 Human can
8	127	10.5	724	8	ABO84902 Human can
9	127	10.5	780	8	ADI82549 Human mod
10	126.5	10.5	839	5	AU86145 Human PRO
11	126.5	10.5	839	5	ABG34056 Human PRO
12	126.5	10.5	839	6	ADA01322 Human PRO
13	126.5	10.5	839	6	ADA43751 Human PRO
14	126.5	10.5	839	6	ADA43519 Human sec
15	126.5	10.5	839	6	ADA01194 Human PRO
16	126.5	10.5	839	7	ADA01078 Human sec
17	126.5	10.5	839	7	ADA43635 Human sec
18	126.5	10.5	839	7	ADA06897 Human PRO
19	126.5	10.5	839	7	ADA08385 Novel hum
20	126.5	10.5	839	7	ADB99678 Human PRO
21	126.5	10.5	839	7	ADB86961 Human PRO
22	126.5	10.5	839	7	ADB66116 Human sec
23	126.5	10.5	839	7	ADB99794 Human PRO
24	126.5	10.5	839	7	ADB99449 Novel hum
25	126.5	10.5	839	7	ADB66000 Human sec

26	126.5	10.5	839	7	ADC23398	Adc23398 Human tra
27	126.5	10.5	839	7	ADC26091	Adc26091 Human PRO
28	126.5	10.5	839	7	ADE04918	Ade04918 Human PRO
29	126.5	10.5	839	7	ADE11224	Ade11224 Human PRO
30	126.5	10.5	839	7	ADD88155	Add88155 Human PRO
31	126.5	10.5	839	7	ADD95450	Add95450 Human sec
32	126.5	10.5	839	7	ADE06380	Ade06380 Human PRO
33	126.5	10.5	839	7	ADE38155	Ade38155 Human PRO
34	126.5	10.5	839	7	ADD88271	Add88271 Human PRO
35	126.5	10.5	839	7	ADD90852	Add90852 Human sec
36	126.5	10.5	839	7	ADF99407	Adf99407 Human sec
37	126.5	10.5	839	7	ADG06500	Adg06500 Human PRO
38	126.5	10.5	839	7	ADG05451	Adg05451 Human PRO
39	126.5	10.5	839	7	ADG82452	Adg82452 Human PRO
40	126.5	10.5	839	7	ADJ37317	Adj37317 Human cum
41	126.5	10.5	839	8	ADE51705	Ade51705 Human sec
42	126.5	10.5	839	8	ADE51821	Ade51821 Human sec
43	126.5	10.5	839	8	ADE37679	Ade37679 Human sec
44	126.5	10.5	839	8	ADE37563	Ade37563 Human sec
45	126.5	10.5	839	8	ADD95334	Add95334 Human sec

ALIGNMENTS

RESULT 1

AAY25337
ID AAY25337 standard; protein; 235 AA.

AC AAY25337;

DT 03-SEP-1999 (first entry)

DE VZV VP26 protein.

KW VP26; immunoreactive protein; immunoassay; detection; anti-VZV; antibody.

OS Human herpesvirus 3.

PN DE19757765-A1.

PD 24-JUN-1999.

PF 23-DEC-1997; 97DE-01057765.

PR 23-DEC-1997; 97DE-01057765.

PA (DADE-) DADE BEHRING MARBURG GMBH.

PI Eickmann M, Gicklhorn D, Radsak K, Hauser H, Giesendorf B;

DR WPI; 1999-359931/31.

DR N-PSDB; AAX78759.

PT Varicella zoster virus VP26 peptide - and corresponding nucleic acid, useful for diagnosis of VZV infections.

PS Claim 3; Page 4; 12pp; German.

CC This invention describes a novel immunoreactive peptide comprising amino acids 12-235 of varicella zoster virus (VZV) protein VP26, and a nucleic acid encoding the peptide. Also claimed is a nucleic acid corresponding to a defined DNA sequence of 705 bp given in the specification, coding for amino acids 1-235 of VZV VP26. The peptide can be used in immunoassays for detecting anti-VZV antibodies. The nucleic acid can be used in hybridisation assays for detecting VZV

SQ Sequence 235 AA;

Query Match 100.0%; Score 1206; DB 2; Length 235;

Best Local Similarity 100.0%; Pred. No. 6e-88;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTQPASSRVVFPSPNPTTFSVEAIAAYTPVALIRLLNASGPLOQGHRTDIADARSITYTVG	60
Db	1	MTQPASSRVVFPSPNPTTFSVEAIAAYTPVALIRLLNASGPLOQGHRTDIADARSITYTVG	60
Qy	61	AAASAARARANHNANTIRRTAMFAETDPMTWLRPTVGLKRTFNPIIRPOPNPNSLGI	120
Db	61	AAASAARARANHNANTIRRTAMFAETDPMTWLRPTVGLKRTFNPIIRPOPNPNSLGI	120
Qy	121	SGPTILPQKTQADOSALQQPAAALAFSGSSPQHPPPTTASVGQQQHVHVGSSGGQPOQ	180
Db	121	SGPTILPQKTQADOSALQQPAAALAFSGSSPQHPPPTTASVGQQQHVHVGSSGGQPOQ	180
Qy	181	GAQSSVTPQTGSPAAAGVPOSTPPPTNTQPGKGQTLSTHGSGGNASRRRV	235
Db	181	GAQSSVTPQTGSPAAAGVPOSTPPPTNTQPGKGQTLSTHGSGGNASRRRV	235

RESULT 2
 ADB70311
 ID ADB70311 standard; protein; 1367 AA.
 XX
 AC ADB70311;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE C. neoformans amino acid sequence SEQ ID NO:3355.
 XX
 KW fungicide; gene therapy; infection.
 XX
 OS Cryptococcus neoformans.
 XX
 PN WO2003052076-A2.
 XX
 PD 26-JUN-2003.
 XX
 PF 17-DEC-2002; 2002WO-US040225.
 XX
 PR 17-DEC-2001; 2001US-0341261P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PT Zamudio C, Eroshkin AM;
 XX
 WI WPI; 2003-533017/50.
 DR N-PSDB; ADB69228.
 XX
 FT New nucleic acid, useful for preparing a composition for treating an
 PT infection caused by Cryptococcus neoformans.
 XX
 PS Claim 9: SEQ ID NO 3355; 136pp; English.

RESULT 3	
ADR08679	
ID	ADR08679 standard; protein; 496 AA.
XX	
XX	ADR08679;
XX	
XX	04-NOV-2004 (first entry)
DT	
XX	
DE	Human protein useful for treating neurological disease Seq 2185.
XX	
XX	human; oligo-capping method; diagnostic marker; gene therapy;
KW	osteoporosis; neurological disease; Alzheimer's disease;
KW	Parkinson's disease; dementia; short memory; cancer;
KW	sense or motor function; emotional reaction; fear response; panic;
KW	osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW	tranquilliser.
XX	
OS	Homo sapiens.
XX	
XX	EPI447413-A2.
PN	
XX	
PD	18-AUG-2004.
XX	
PF	12-FEB-2004; 2004EP-00003145.
XX	
XX	14-FEB-2003; 2003JP-00102207.
PR	09-MAY-2003; 2003JP-00131452.
PR	
XX	(REAS-) RES ASSOC BIOTECHNOLOGY.
PA	
XX	
PI	Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI	Wakamatsu A, Ishii S, Nagai K, Irie R;
XX	
XX	WPI; 2004-583265/57.
DR	
DR	N-PSDB; ADR06723.
XX	
PT	New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT	Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX	
PS	Claim 1; SEQ ID NO 2185; 2686pp; English.
XX	
CC	This invention relates to novel, isolated full length human cDNA
CC	molecules and the encoded proteins thereof. Specifically, it refers to
CC	cDNA clones obtained by an oligo-capping method, where none of these
CC	clones are identical to any known human mRNAs. The present invention
CC	describes an immunoassay to identify agonists and antagonists, as well as
CC	antibodies, antisense molecules and siRNAs that can all be used to bind
CC	to and modulate expression of the cDNA molecules. As such, these
CC	molecules are useful for diagnostic markers or therapeutic targets for
CC	the various diseases or morbid states. In particular, they are useful in
CC	gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC	disease, Parkinson's disease, dementia, short memory and various cancers,
CC	as well as for maintaining equilibrium of sense or motor function, and
CC	for treating emotional reaction, fear response and panic. Accordingly,
CC	they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC	cytostatic and tranquilliser activities. This polypeptide is a protein
CC	encoded by a full length human cDNA sequence of the invention. NOTE: This

CC sequence is not given in the sequence listing of the specification but
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
CC office.
XX
SQ Sequence 496 AA;
Query Match 11.1%; Score 133.5; DB 8; Length 496;
Best Local Similarity 26.1%; Pred. No. 0.033;
Matches 55; Conservative 19; Mismatches 58; Indels 79; Gaps 9;
QY 69 RANHNANTIRRTAMPAETDPMTLRLPTVGLKRTFNPRIRIROPNPMS-----LGISGP- 123
Db 174 KAKGNOPARTGLSRNPPT-----QKPSPPMSGRTLORNTPY 215
QY 124 -TILPQKTSADQSAALAFSGSSPQHPPPTTSASVQOQHVVSGSG----- 175
Db 216 KTLBPVKPTVPNDYMTSPARL--GS--QHSFGRT--ASLNRPTHSGSGSGSREN 268
QY 176 -----QQPQQAQSSTVQPTTGSPPAAQ-----GVQSTP----- 205
Db 269 SGSSSIGIPIAVPTSPPTIGENISVPPPSGAPPPLAPLPLPVSTVIAAPGSAPGSQY 328
QY 206 -----PPTONTPOGGKGOTLSHTGO 225
Db 329 GTMTROIQRHNSSTSSSTSGGRRTPSVTAQ 359

RESULT 4
AAP50073
ID AAP50073 standard; protein; 907 AA.
XX
AC AAP50073;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 17-OCT-1991 (first entry)
XX
DE Epstein-Barr virus (EBV) outer surface protein.
XX
KW Epstein-Barr virus; antigen; vaccine.
XX
OS Human herpesvirus 4.
XX
FN EPI51079-A.
XX
PD 07-AUG-1985.
XX
PF 28-JAN-1985; 8SEP-00400141.
XX
PR 30-JAN-1984; 84US-00575352.
PR 23-JUL-1984; 84US-00633558.
XX
PA (UYCH-) UNIV CHICAGO.
XX
PI Kleff E, Tanner J, Hummel M, Belsel C;
XX
DR WPI; 1985-191978/32.
DR N-PSDB; AAN50114.
XX
PT New fragment of Epstein-Barr Virus DNA - useful in vector to express
PT polypeptide for use in prepn. of vaccine against the virus and for use in
PT diagnosis.
XX
PS Claim 2; Page 23-25; 26pp; English.
XX
CC The sequence encodes an outer surface viral protein of EBV, used to
CC generate antibodies reacting with the surface proteins of EBV-infected
CC cells, and in the preparation of a vaccine against EBV. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 907 AA;

Query Match 10.6%; Score 127.5; DB 1; Length 907;
Best Local Similarity 24.9%; Pred. No. 0.2;
Matches 64; Conservative 26; Mismatches 88; Indels 79; Gaps 14;
QY 2 TQPASSRVFDP--SNPT---TFSVEAIAAYTPVALIRLLNASGLOPQGHVRVDIADARSI 56
Db 577 TSPTSATVTTPTPNATSTLTKTSPTSATVTFP-----NATGP----- 614
QY 57 YTVGAASAARARAHNANTIRRTAMPATDPMPTWLRPTVGLKRTFNPRIRIROPNPMS 116
Db 615 -TVGETSPQANA-TNH--TLGGTS-----PT-----PVTSPQKNATS 648
QY 117 SLGISGPTILPQKTSADQSAALQAPAL--AFSGSSPQHPP-----PQTSA 161
Db 649 AVTTGQHNTTSSSTSSMLRPNPSTLSPSTSONSTSHMPLLSAHTPGENITQVTPA 708
QY 162 SVGQQQHVVSQSQQQPQQAQSSTVOP---TTGSPPAAGVPOSTPTPTQNTPOGGKXG 218
Db 709 SI--STHHVSTSS-PEPRPGTTTQASGSGNSSTSTKGEVNVTKGTPPQNATSPQAPSG 765
QY 219 -----TLSHTGQSGNAS 230
Db 766 KTAVPTVTSTGKANST 782
RESULT 5
AAR80144
ID AAR80144 standard; protein; 907 AA.
XX
AC AAR80144;
XX
DT 16-OCT-2003 (revised)
DT 18-JAN-1996 (first entry)
XX
DE EBV gp350/220.
XX
KW EBV; gp350; gp220; gp350/gp220; non-splicing variant; vaccine.
XX
OS Human herpesvirus 4.
XX
FN Key Location/Qualifiers
FT Peptide 1..18
FT /label= Sig_peptide
FT Region 861..881
FT /note= "transmembrane region"
XX
FN WO9528488-A1.
XX
PD 26-OCT-1995.
XX
PF 13-APR-1995; 95WO-US004611.
XX
PR 18-APR-1994; 94US-00229291.
XX
PA (AVIR-) AVIRON.
XX
PI Spaete R, Jackman WT;
XX
DR WPI; 1995-373802/48.
DR N-PSDB; AAT04821.
XX
PT New DNA encoding a homogeneous gp350 protein - can be used for preventing
PT and treating Epstein-Barr virus-related diseases or conditions.
XX
PS Disclosure; Fig 1; 61pp; English.
XX
CC The donor and acceptor splice sites of the EBV gene encoding gp350/ 220
CC are mutated by replacement of native nucleotides by non-native
CC nucleotides, without altering the encoded amino acid sequence, resulting
CC in elimination of gp220 prodn. Recombinant homogeneous gp350, useful in
CC vaccines, is expressed in mammalian or insect cell hosts. (Updated on 16-
CC OCT-2003 to standardise OS field)
XX

SQ Sequence 907 AA;

Query Match 10.6%; Score 127.5; DB 2; Length 907;
Best Local Similarity 24.9%; Pred. No. 0.2;
Matches 64; Conservative 26; Mismatches 88; Indels 79; Gaps 14;

QY 2 TOPASSRVVFD--SNPT---TFSVEAIAAYTPVALIRLLNASGPIQPGHVRVDIADARSI 56
DB 577 TSPTSAVTTPTTNPATSPTLGKTSPTSAVTTPTP-----NATGP----- 614

QY 57 YTVGAASAARARANNANTIRRTAMFAETDPMWLRPTVGLKRTFNPRIIRPQPPNPSM 116
DB 615 -TVGETSPQANA-TNH---TLGGS-----PT-----PVTSPQPNKATS 648

QY 117 SLGISGPTILPQKTSQADQSALQQPAAL--AFSGSSPQHPP-----PQTSA 161
DB 649 AVTTGQHNTSSSTSSMSLRPSSNPETLSPTSDNSTSHMPLLTSAHPTGGENITQVTPA 708

QY 162 SVGQQQHVHVGSSGQQPQOQAGSSTVQP---TTGSPPAAGVPOSTPPPTQNTPTQGGKQ 218
DB 709 SI--STHHVSTSS-PEPRFGTTSQASGPGNSSTSTKPGEVNVTGTPPQNATSPQAPSGQ 765

QY 219 -----TLSHTGSGGNAS 230
DB 766 KTAVPTVTSTGGKANST 782

RESULT 6
AA168009
ID AAY68009 standard; protein; 907 AA.
AC AAY68009;
DT 06-AUG-2003 (revised)
DT 11-APR-2000 (first entry)
DE Epstein-Barr virus major outer envelope glycoprotein Gp350.
KW Epstein-Barr virus; major outer envelope glycoprotein; Gp350; Gp220;
KW B cell activation; immunoglobulin; secretion; EBV; Gp350/220; antigen;
KW vaccine; adjuvant; fusion protein; antimicrobial; antiviral; CR2; CD21;
KW anti-allergic; antitumour; immunostimulatory; infection; tumour;
KW complement receptor 2.
OS Human herpesvirus 4.
XX
XX WO9964603-A2.
XX
XX 16-DEC-1999.
XX
XX 10-JUN-1999; 99WO-US013113.
XX
XX 12-JUN-1998; 98US-0089158P.
XX
XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PA (MOND/) MOND J J.
PA (LEES/) LEES A.
XX
XX Mond JJ, Lees A;
XX
XX WPI; 2000-116546/10.
XX
XX Adjuvant containing an Epstein-Barr virus sequence that binds to
PT complement receptor 2, for protecting against, e.g. infection or tumors.
PT
XX
PS Disclosure; Fig 1A; 43pp; English.
XX
XX The present invention describes an adjuvant (A) comprising at least one
CC EBV (Epstein-Barr virus) Gp350/220 sequence (I) that binds to CR2
CC (complement receptor 2; CD21). Vaccines containing (A) and at least one
CC other antigenic epitope (also similar immunogens and nucleic acid vectors
CC that express (I)) are used to elicit an antibody response to both (I)
CC (for protection against EBV) and the second epitope, which may be

CC associated with some other infectious agent, allergen, tumour antigen or
CC generally any condition that requires immune stimulation. The vaccines
CC and immunogens may also be used to treat B cells in vitro. (A) increases
CC the immunogenicity of a co-administered antigen. By combining (I), a non-
CC specific B cell stimulator, with another antigen, the stimulatory effect
CC is targeted to antigen-specific B cells, i.e. B cells that secrete
CC immunoglobulins specific for the antigen and through (I)-mediated crosslinking of
CC through the antigen receptor and through (I)-mediated crosslinking of
CC CR2. Constructs of (I) and second antigen are relatively small, so should
CC be cleared relatively quickly (reducing immunogenicity) and many copies
CC of second antigen can be included to increase antigenicity. The need for
CC expensive anti-CR antibodies and potentially inflammatory C3 components
CC is avoided and folding of the CR2-binding domain in (I)-antigen fusion
CC proteins is unlikely to be disrupted. The present sequence represents EBV
CC major outer envelope glycoprotein Gp350. (Updated on 06-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 907 AA;

Query Match 10.6%; Score 127.5; DB 3; Length 907;
Best Local Similarity 24.9%; Pred. No. 0.2;
Matches 64; Conservative 26; Mismatches 88; Indels 79; Gaps 14;

QY 2 TOPASSRVVFD--SNPT---TFSVEAIAAYTPVALIRLLNASGPIQPGHVRVDIADARSI 56
DB 577 TSPTSAVTTPTTNPATSPTLGKTSPTSAVTTPTP-----NATGP----- 614

QY 57 YTVGAASAARARANNANTIRRTAMFAETDPMWLRPTVGLKRTFNPRIIRPQPPNPSM 116
DB 615 -TVGETSPQANA-TNH---TLGGS-----PT-----PVTSPQPNKATS 648

QY 117 SLGISGPTILPQKTSQADQSALQQPAAL--AFSGSSPQHPP-----PQTSA 161
DB 649 AVTTGQHNTSSSTSSMSLRPSSNPETLSPTSDNSTSHMPLLTSAHPTGGENITQVTPA 708

QY 162 SVGQQQHVHVGSSGQQPQOQAGSSTVQP---TTGSPPAAGVPOSTPPPTQNTPTQGGKQ 218
DB 709 SI--STHHVSTSS-PEPRFGTTSQASGPGNSSTSTKPGEVNVTGTPPQNATSPQAPSGQ 765

QY 219 -----TLSHTGSGGNAS 230
DB 766 KTAVPTVTSTGGKANST 782

RESULT 7
ABO84900
ID ABO84900 standard; protein; 634 AA.
XX
XX ABO84900;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human cancer-associated protein (CAP) HP07-062.
XX
XX Human; cancer-associated protein; CAP; cancer; cytostatic.
XX
XX Homo sapiens.
XX
XX WO2004058146-A2.
XX
XX 15-JUL-2004.
XX
XX 15-DEC-2003; 2003WO-US040081.
XX
XX 17-DEC-2002; 2002US-00322281.
XX
XX (SAGR-) SAGRES DISCOVERY INC.
XX
XX Morris DW, Malandro MS;
XX
XX WPI; 2004-499109/47.
XX
XX N-PSDB; ABD33344.
XX

XX PF 09-JUL-2003; 2003WO-US021510.
XX PR 10-JUL-2002; 2002US-0394795P.
PR 17-AUG-2002; 2002US-0401739P.
PR 16-SEP-2002; 2002US-0411010P.
PR 30-DEC-2002; 2002US-0437158P.
XX PA (EXEL-) EXELIXIS INC.
XX PI Francis-Lang H, Friedman L, Kidd T, Roche S, Joo DM, Lickteig K;
PI Amundsen CD, Hai B, Zhang H, Adamkewicz JI, Hammonds GR;
XX DR WPI; 2004-091358/09.
DR N-PSDB; ADI82488.
XX PT Identifying a candidate p21 pathway modulating agent, useful for treating
PT a disease such as cancer, comprises contacting an assay system comprising
PT a MP21 polypeptide or nucleic acid with a test agent.
XX PS Example 2; SEQ ID NO 115; 392pp; English.
XX CC This invention relates to a novel candidate p21 pathway modulating agent
CC by contacting an assay system comprising an MP21 (modifier of p21)
CC polypeptide or nucleic acid with a test agent, where in the absence of
CC the test agent the system provides a reference activity and detecting a
CC test agent-biased activity of the assay system. The invention may be
CC useful for the production of compounds with a cytostatic activity through
CC modulation of MP21 protein activity. The MP21 polypeptide or nucleic acid
CC can be used for identifying MP21 modulating agents useful as therapeutic
CC targets for diagnosing cancer or treating disorders associated with
CC defective or impaired p21 and/or MP21 function. MP21 modulating agents
CC are useful in diagnosis, therapy, for example treating cancer, and
CC pharmaceutical development. The genetically modified animals may be used
CC for in vivo assays to test for activity of a candidate p21 modulating
CC agent, or to further assess the role of MP21 in a p21 pathway process.
CC The present sequence is that of a human MP21 protein which is an
CC orthologue of a Drosophila p21 modifier and which was used in the
CC exemplification of the invention.
XX SQ Sequence 780 AA;

Query Match 10.5%; Score 127; DB 8; Length 780;
Best Local Similarity 26.3%; Pred. No. 0.19;
Matches 68; Conservative 17; Mismatches 106; Indels 68; Gaps 12;
QY 1 MTQPASSRVVFPNSNTTTSVEAIAAYTPVALIRLNLNASGPLOP-----GHRVDIADAR 54
DB 258 MSQPT-----PAQPSFSGVGPQPPPPVGVGAVQAQSSAPLPPFPFGAATGFPQPMMAAQ 310
QY 55 SIYTVGAASAARARAHNANTIRRTAMFAETDPTMTLRLPTVGLKRTFNP-RIIRPQPN 113
DB 311 PSQPQAGGGQTLPTTN--VTLAQPAMSLPQP-----GPAVGAPAAQPPQFAPQPOI 364
QY 114 PMSLIGISGFTLPKQTSADQSALQOAPALAFSGSSQHP-----PPOTTSASVQO 165
DB 365 PGHLL-----LP--VQPSGGSEYIQHVAGLQPPSPAQPSSTGAASAPATAATLPVGT 415
QY 166 QHVS-----GSSGQ-----PQGAQSSVTQPTTQSP-----PAAQ 198
DB 416 GQNASVGAQLMGASSQPSSEAMAPRTGPAQGGQVAPCQPTGVPPTVGVVQPCLGPA 475
QY 199 GVPQSTPTPTQNTPQGGK 217
DB 476 GQPSVFP-----QMGSG 490

RESULT 10
ID AAU86145
XX AAU86145 standard; protein; 839 AA.
AC AAU86145;
XX

DT 15-JUL-2002 (first entry)
XX Human PRO7168 polypeptide.
DE
XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoealic disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
KW neuroprotective.
OS Homo sapiens.
XX WO200153486-A1.
XX 26-JUL-2001.
XX 11-FEB-2000; 2000WO-US003565.
XX 08-MAR-1999; 99WO-US005028.
PR 11-MAR-1999; 99US-0123972P.
PR 11-MAY-1999; 99US-0133459P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 22-JUN-1999; 99US-0140653P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149395P.
PR 31-AUG-1999; 99US-0151689P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 05-JAN-2000; 2000WO-US000219.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX WPI; 2002-205567/26.
DR N-PSDB; ABK40271.
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX Claim 61; Fig 36; 302pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The PRO
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC stromal and blastocoealic disorders, inflammatory, immune and angiogenic
CC disorders. The polynucleotide sequences are also useful in gene therapy.
CC AAU86128-AAU86162 represent the human PRO polypeptides of the invention
XX
SQ Sequence 839 AA;

Query Match 10.5%; Score 126.5; DB 5; Length 839;
Best Local Similarity 25.5%; Pred. No. 0.22;
Matches 76; Conservative 24; Mismatches 97; Indels 101; Gaps 16;
QY 17 TTFSVEAIAA-----YTPVALIR-----LLNASGPLOP-----GHRVDIADARS 55
DB 338 TQVTVEAANAAGSPRPFQPSLYRGTVARGAGAGVGVVVKDAAPSPQLRIQAQDPFSDLNS 397
QY 56 IYT-----VGAASAAARA-----NHN-----ANTIRRTAMFAETDP 88
DB 398 AIYIRITNHSRMEGVEVLLTTTLAQAGAFYAEVEAHNTVTSGTATTVIEIQVSEQEPP 457

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QY      89 MTWLRPTVGLKRTFNRIIRPQPPNSM-----SLGISGP-----TILPKQTKOS----- 132
D      458 STEAGGTTGPMWTTTSEV--PRPPEPSQSPSTSSCGGTGPHPPSGTTLRPPTSTPGGP 515
QY      133 --ADQSALQQPAALAFSGSSSQHPHPPQT-----SASVQQQHHVSSGSGQQPQQGAQ 183
D      516 PGAENSTSHQPATP--GGDTAQTPKPGTSQPMPPGVGTSTSHQPATPSGGTAQTPEPGTS 573
QY      184 -----SSTVQPTTGSPPAAQ-----GVPQSTPP-----PTQNTPQGGKGQT 219
D      574 QPMPPSMGTSTSHQPATPGGTAQTPEAGTSQPMPPGMPGTSTSHQPT--TFGGSTAQT 629

RESULT 11
ID      ABG34056
XX      ABG34056 standard; protein; 839 AA.
AC      ABG34056;
DT      15-JUL-2002 (first entry)
DE      Human Pro peptide #27.
KW      Human; PRO; secreted protein; transmembrane protein; genetic disorder;
KW      tumour; cancer.
OS      Homo sapiens.
PN      WO200224888-A2.
XX      PD
XX      28-MAR-2002.
XX      29-AUG-2001; 2001WO-US027099.
XX      01-SEP-2000; 2000US-0229896P.
XX      05-SEP-2000; 2000US-0230621P.
XX      22-SEP-2000; 2000US-0235147P.
XX      10-NOV-2000; 2000WO-US030873.
XX      12-JAN-2001; 2001US-0261878P.
XX      16-JAN-2001; 2001US-0261910P.
XX      16-JAN-2001; 2001US-0261939P.
XX      16-JAN-2001; 2001US-0262150P.
XX      25-JAN-2001; 2001US-0264395P.
XX      02-FEB-2001; 2001US-0266421P.
XX      09-FEB-2001; 2001US-0267623P.
XX      28-FEB-2001; 2001WO-US006520.
XX      09-MAR-2001; 2001US-0274399P.
XX      03-APR-2001; 2001US-0280982P.
XX      04-APR-2001; 2001US-0282129P.
XX      04-APR-2001; 2001US-0282199P.
XX      09-MAY-2001; 2001US-0290589P.
XX      25-MAY-2001; 2001WO-US017092.
XX      01-JUN-2001; 2001WO-US017800.
XX      20-JUN-2001; 2001WO-US019692.
XX      29-JUN-2001; 2001WO-US021066.
XX      09-JUL-2001; 2001WO-US021735.
XX      (GETH ) GENENTECH INC.
XX      Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI      Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
PI      Fong S;
XX      WPI; 2002-362426/39.
XX      DR N-PSDB; ABK69987.
XX      New PRO polypeptides and polynucleotides encoding the polypeptides,
PT      useful in gene therapy, chromosome identification, tissue typing, or for
PT      genetic analysis of individuals with genetic disorders.
XX      Claim 11; Fig 54; 218pp; English.
XX
```

```
CC      This invention relates to the cDNA and protein sequences of novel
CC      secreted and transmembrane polypeptides PRO polypeptides. The invention
CC      also comprises a method for producing the proteins of the invention by
CC      recombinant means and antibodies specific for the protein of the
CC      invention. The antibody may be used for detecting the PRO proteins of the
CC      invention and may be used to modify their activity. polynucleotides may
CC      be used as hybridisation probes for a cDNA library to isolate the full-
CC      length PRO cDNA or to isolate other cDNAs, to construct hybridisation
CC      probes for mapping the gene which encodes that PRO and for genetic
CC      analysis of individuals with genetic disorders, in assays to identify
CC      other proteins or molecules involved in binding reaction, to generate
CC      transgenic animals or knock-out animals which in turn are useful in the
CC      development and screening of therapeutically useful reagents, for
CC      chromosome identification, and tissue typing. The PRO polypeptides are
CC      useful in gene therapy, and as molecular weight markers for protein
CC      electrophoresis purposes. The sequences may also be used to detect
CC      overexpression on PRO polypeptides in cancerous tumours and for screening
CC      for differentially expressed genes using microarray technology. The
CC      present sequence represents a human PRO protein of the invention
XX
SQ      Sequence 839 AA;
      Query Match      10.5%; Score 126.5; DB 5; Length 839;
      Best Local Similarity      25.5%; Pred. No. 0.22;
      Matches 76; Conservative 24; Mismatches 97; Indels 101; Gaps 16;
QY      17 TTFSEVETAA-----YTPVALIR-----LLNASGLPQP-----GHRVDIADARS 55
D      338 TQVTVEAVAAAGSPRPFPQSLYRGTVARGAGVGVVXDAAPSQPLRIQAQDPFSDLNS 397
QY      56 IYT-----VGAASAARARA-----NHN-----ANTIRTMFAETDP 88
D      398 AITYRIITNHSFRMEGEVLTTLTLAGAGAFYAEVAHNTVTSGTATTVIBIQVSEQPP 457
QY      89 MTWLRPTVGLKRTFNRIIRPQPPNSM-----SLGISGP-----TILPKQTKOS----- 132
D      458 STEAGGTTGPMWTTTSEV--PRPPEPSQSPSTSSCGGTGPHPPSGTTLRPPTSTPGGP 515
QY      133 --ADQSALQQPAALAFSGSSSQHPHPPQT-----SASVQQQHHVSSGSGQQPQQGAQ 183
D      516 PGAENSTSHQPATP--GGDTAQTPKPGTSQPMPPGVGTSTSHQPATPSGGTAQTPEPGTS 573
QY      184 -----SSTVQPTTGSPPAAQ-----GVPQSTPP-----PTQNTPQGGKGQT 219
D      574 QPMPPSMGTSTSHQPATPGGTAQTPEAGTSQPMPPGMPGTSTSHQPT--TFGGSTAQT 629

RESULT 12
ADA01322
ID      ADA01322 standard; protein; 839 AA.
XX      AC
XX      ADA01322;
XX      06-NOV-2003 (first entry)
XX      Human PRO polypeptide #27.
XX      Human; PRO; secreted polypeptide; transmembrane polypeptide;
XX      tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW      adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW      microvascular endothelial cell; endothelial cell tube formation;
KW      sports-related joint problem; articular cartilage defect; osteoarthritis;
KW      rheumatoid arthritis; osteopahtic; antirheumatic; antiarthritic.
XX      OS
XX      Homo sapiens.
XX      FN
XX      US2003068779-A1.
XX      PD
XX      10-APR-2003.
XX      PF
XX      16-SEP-2002; 2002US-00245107.
XX      09-MAY-2001; 2001US-0290589P.
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Search completed: September 25, 2005, 20:55:23
Job time : 328 secs

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PD 10-APR-2003.
XX
XX PF
XX 16-SEP-2002; 2002US-00245851.
XX
XX 27-APR-1999; 99US-0131271P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
XX WPI; 2003-625487/59.
DR N-PSDB; ADA01193.
XX
XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX
XX Claim 11; Fig 54; 308pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, kidney and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for stimulating and inhibiting proliferation of human
CC microvascular endothelial cells and for inducing endothelial cell tube
CC formation. This sequence represents a human PRO polypeptide of the
XX invention.
XX
XX Sequence 839 AA;
XX
Query Match 10.5%; Score 126.5; DB 6; Length 839;
Best Local Similarity 25.5%; Pred. No. 0.22;
Matches 76; Conservative 24; Mismatches 97; Indels 101; Gaps 16;
QY 17 TTFSEVAIRA-----YTPVALIR-----LLNAGSLPQ-----GHRVDIADARS 55
Db 338 TQVTVEAAGAAGSPRPFQSLYRGTVARGAGAGVVKDAAPSQLRIQAQDPEFSDLNS 397
QY 56 IYT-----VGAASAARARA-----NHN-----ANTIRRTAMFAETDP 88
Db 398 AITYRITNHSHERMEGEVLTITLQAQAGAFYAEVAENHTVTSQTATTVEIQVSEQEP 457
QY 89 MTWLRPTVGLKRTFNRIIRPQNPMS-----SIGISGP-----TILPQKTQS----- 132
Db 458 STEAGGTTGPWTSTSEV--PRPEPSQSPSTSSGGTGPHPPGSTTLRPPTSTSPGGP 515
QY 133 --ADQNALQPAALAFSGSSPHPPQTT-----SASVGQOQHVVSGSSGQPOQGAQ 183
Db 516 PGAENSTSHQATP--GGDTAQTPKPGTSQMPFPGVGTSTSHQATPFGSGTAQTPEPGTS 573
QY 184 -----SSTVQPTTGSPPAAQ-----GVPQSTTP-----PTQNTPOGKGQT 219
Db 574 QPMPPSNGTSTSHQATPFGGTAQTPEAGTSQMPFPGMGTSTSHQPT--TPGGGTAQT 629
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 25, 2005, 18:22:58 ; Search time 389 Seconds
(without alignments)
309.354 Million cell updates/sec

Title: US-09-874-140-2

Perfect score: 1206

Sequence: 1 MTQPASRRVDPSPNPTTFS.....KGQTLSTGSGNASRRRV 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	235	1 VP26_VZVD	P09279 varicella-z
2	1206	100.0	235	1 Q6QCN2	Q6qcn2 human herpe
3	473.5	39.3	228	2 Q9E123	Q9e123 cercopithec
4	175	14.5	124	2 Q65554	Q65554 bovine herp
5	175	14.5	124	2 Q77CD3	Q77cd3 bovine herp
6	174	14.4	103	2 Q77KA6	Q77ka6 suid herpes
7	174	14.4	103	2 Q77KCS6	Q77kcs6 pseudorabie
8	173	14.3	125	2 Q6X247	Q6x247 bovine herp
9	154.5	12.8	119	2 Q39267	Q39267 equid herpe
10	153.5	12.7	119	1 VP26_BHV1B	P28974 equine herp
11	153.5	12.7	119	2 Q6S6F6	Q6s6p6 equid herpe
12	142	11.8	503	2 Q66IV2	Q66iv2 xenopus lae
13	141.5	11.7	771	2 Q76N76	Q76n76 rattus norv
14	139	11.5	1114	2 Q6P9L3	Q6p9l3 mus musculu
15	138	11.4	776	2 Q9JJ50	Q9jj50 rattus norv
16	133.5	11.1	508	1 AB11_HUMAN	Q81zp0 homo sapien
17	132.5	11.0	165	2 Q9DPQ4	Q9dpq4 meleagrid h
18	132.5	11.0	237	2 Q9E1F9	Q9e1f9 meleagrid h
19	132	10.9	862	1 MCML_RAT	Q9jik1 rattus norv
20	131.5	10.9	2232	2 Q81FX6	Q81fx6 caenorhabdi
21	131	10.9	530	1 NLFA_MOUSE	Q8bg30 mus musculu
22	129.5	10.7	686	2 Q750F3	Q750f3 neurospora
23	128	10.6	1151	2 Q57580	Q57580 gallus gall
24	127.5	10.6	907	2 Q65537	Q65537 human herpe
25	127	10.5	721	1 YK82_MYCTU	Q10690 mycobacteri
26	127	10.5	721	1 Q7T224	Q7tz24 mycobacteri
27	127	10.5	780	2 Q6P150	Q6p150 homo sapien
28	127	10.5	784	2 Q90YB5	Q90yb5 gallus gall
29	127	10.5	825	2 Q75157	Q75157 homo sapien
30	127	10.5	829	2 Q6N5Q1	Q6n5q1 rhodospseudo
31	126.5	10.5	2321	2 Q6R5R1	Q6r5r1 meleagrid h

32 126.5 10.5 2321 2 Q9DGT6 Q9dgt6 meleagrid h
33 126.5 10.5 2323 2 Q6HAA3 Q6haa3 meleagrid h
34 126 10.4 775 2 Q99LI8 Q99li8 mus musculu
35 126 10.4 775 2 Q61691 Q61691 mus musculu
36 125.5 10.4 70 2 Q8U210 Q8u210 pseudorabie
37 125.5 10.4 647 2 Q9VQF3 Q9vqf3 drosophila
38 125.5 10.4 760 1 HRS_DROME Q960x8 drosophila
39 125.5 10.4 783 2 Q91331 Q91331 cercopithec
40 125.5 10.4 800 2 Q6CGD7 Q6cgd7 yarrowia li
41 125.5 10.4 2169 2 Q8NPN6 Q8npn6 corynebacte
42 125 10.4 1061 2 Q9V853 Q9v853 drosophila
43 125 10.4 1724 2 P91019 P91019 caenorhabdi
44 124.5 10.3 131 2 Q9E6N4 Q9e6n4 meleagrid h
45 124.5 10.3 513 2 Q9FTT8 Q9ftt8 oryza sativ

ALIGNMENTS

RESULT 1
ID VP26_VZVD STANDARD; PRT; 235 AA.
AC P09279;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Capsid protein VP26.
GN Name=23;
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10338;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86306657; PubMed=3018124;
RA Davison A.J., Scott J.E.;
RT "The complete DNA sequence of varicella-zoster virus.";
RL J. Gen. Virol. 67:1759-1816(1986).
CC -!- SIMILARITY: Belongs to the herpesviruses UL35 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

CC EMBL; X04370; CAA27906.1; -.
DR PIR; E27343; WZBE23.
DR InterPro; IPR007584; UL35.
DR Pfam; PF04496; Herpes_UL35; 1.
KW Coat protein.
SQ SEQUENCE 235 AA; 24417 MW; 6BC37A7BEE06F30A CRC64;
Query Match 100.0%; Score 1206; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 9.5e-64;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQPASRRVDPSPNPTTFSVEAIAAYTPVALIRLLNAGPLQGHVRVDIADARSITYTVG 60
DB 1 MTQPASRRVDPSPNPTTFSVEAIAAYTPVALIRLLNAGPLQGHVRVDIADARSITYTVG 60
QY 61 AAAGAAARARAHNANTIRRTAMFAETDPMTWLRTVGLKRTFNPRRIIRPQPNPMSLGI 120
DB 61 AAAGAAARARAHNANTIRRTAMFAETDPMTWLRTVGLKRTFNPRRIIRPQPNPMSLGI 120
QY 121 SGPTILPQKTQADQALQQAALAFSGSSPOHPPPTTSASVGGQHHVSGSSQQPQQ 180
DB 121 SGPTILPQKTQADQALQQAALAFSGSSPOHPPPTTSASVGGQHHVSGSSQQPQQ 180
QY 181 GAQSTVPTTGPAAAGVQSPPTPTNTPOGKGQTLSTGSGNASRRRV 235
DB 181 GAQSTVPTTGPAAAGVQSPPTPTNTPOGKGQTLSTGSGNASRRRV 235


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DR EMBL; Z78205; CAB01606.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR007584; UL35.
DR Pfam; PF04496; Herpes_UL35; 1.
SQ SEQUENCE 124 AA; 13420 MW; 31FF6C0DFA43CD81 CRC64;

Query Match 14.5%; Score 175; DB 2; Length 124;
Best Local Similarity 36.3%; Pred. No. 0.0022;
Matches 41; Conservative 18; Mismatches 48; Indels 6; Gaps 3;

Qy 1 MTQPASSRVVDPGNTTFSVEAIAAYTPVALIRLLNASG-PLOGGHRVD-IADARSIYT 58
Db 1 MSAPAG-----IDRPAPATITPTDRLDLPVQILHLVNAARPLQDGTTPQVSARRNLL 56

Qy 59 VGAASAARARANHNANTIRRTAMPAETDPMTWLPTVGLKRTFNPRIIRPOP 111
Db 57 VGTSLAMVDLRRRHEKAVVPVPWFATYDHAHWARTIGLKRTFLPRVQLPP 109

RESULT 5
Q77CD3 PRELIMINARY; PRT; 124 AA.
AC Q77CD3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein.
GN Name=UL35;
OS Bovine herpesvirus type 1.1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=79889;
RN SEQUENCE FROM N.A.
RA Schwytzer M., Vlcek C., Lowery D.E., Bello L.J., Meyer G., Misra V.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE FROM N.A.
RA Schwytzer M., Paces V., Letchworth G.J., Misra V., Buhk H.J.,
RA Lowery D.E., Simard C., Bello L.J., Thiry E., Vlcek C.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ004801; CAA06098.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR007584; UL35.
DR Pfam; PF04496; Herpes_UL35; 1.
SQ SEQUENCE 124 AA; 13420 MW; 31FF6C0DFA43CD81 CRC64;

Query Match 14.5%; Score 175; DB 2; Length 124;
Best Local Similarity 36.3%; Pred. No. 0.0022;
Matches 41; Conservative 18; Mismatches 48; Indels 6; Gaps 3;

Qy 1 MTQPASSRVVDPGNTTFSVEAIAAYTPVALIRLLNASG-PLOGGHRVD-IADARSIYT 58
Db 1 MSAPAG-----IDRPAPATITPTDRLDLPVQILHLVNAARPLQDGTTPQVSARRNLL 56

Qy 59 VGAASAARARANHNANTIRRTAMPAETDPMTWLPTVGLKRTFNPRIIRPOP 111
Db 57 VGTSLAMVDLRRRHEKAVVPVPWFATYDHAHWARTIGLKRTFLPRVQLPP 109

RESULT 6
Q77KA6 PRELIMINARY; PRT; 103 AA.
AC Q77KA6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE UL35 protein.
GN Name=UL35;
OS Suid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10345;
```

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RN SEQUENCE FROM N.A.
RP STRAIN=Becker;
RX MEDLINE=21145867; PubMed=11248101; DOI=10.1073/pnas.061029798;
RA Smith G.A., Gross S.P., Enquist L.W.;
RT "Herpesviruses use bidirectional fast-axonal transport to spread in
sensory neurons.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3466-3470 (2001).
DR EMBL; AF301599; AAG21381.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR007584; UL35.
DR Pfam; PF04496; Herpes_UL35; 1.
SQ SEQUENCE 103 AA; 11474 MW; 0B8757DB8B7B0ECC CRC64;

Query Match 14.4%; Score 174; DB 2; Length 103;
Best Local Similarity 37.1%; Pred. No. 0.0021;
Matches 39; Conservative 17; Mismatches 41; Indels 8; Gaps 3;

Qy 11 FDPSPNTTFSVEAIAAYTPVALIRLLNASGFLQ-----PGRVDIADARSIVTGAASAA 66
Db 3 FDPNNPTITTAQTLLEGALPVDILRLNRATGLQMDAAEAHAI-VEDARRTLFIGTSLALV 61

Qy 67 RARAHNANTIRRTAMPAETDPMTWLPTVGLKRTFNPRIIRPOP 111
Db 62 NLRHAKHLIVERQPMFATSDYSSWARPTVGLKRTFCP---RPPP 103

RESULT 7
Q91CS6 PRELIMINARY; PRT; 103 AA.
AC Q91CS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE UL35 protein.
GN Name=UL35;
OS Pseudorabies virus (strain Kaplan) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=33703;
RN SEQUENCE FROM N.A.
RP STRAIN=Kaplan;
RX MEDLINE=20481646; PubMed=11024135;
RX DOI=10.1128/JVI.74.21.10663-10073.2000;
RA Klupp B.G., Granzow H., Mettenleiter T.C.;
RT "Primary envelopment of pseudorabies virus at the nuclear membrane
requires the UL34 gene product.";
RL J. Virol. 74:10063-10073 (2000).
DR EMBL; AJ276165; CAB98182.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR007584; UL35.
DR Pfam; PF04496; Herpes_UL35; 1.
SQ SEQUENCE 103 AA; 11474 MW; 0B8757DB8B7B0ECC CRC64;

Query Match 14.4%; Score 174; DB 2; Length 103;
Best Local Similarity 37.1%; Pred. No. 0.0021;
Matches 39; Conservative 17; Mismatches 41; Indels 8; Gaps 3;

Qy 11 FDPSPNTTFSVEAIAAYTPVALIRLLNASGFLQ-----PGRVDIADARSIVTGAASAA 66
Db 3 FDPNNPTITTAQTLLEGALPVDILRLNRATGLQMDAAEAHAI-VEDARRTLFIGTSLALV 61

Qy 67 RARAHNANTIRRTAMPAETDPMTWLPTVGLKRTFNPRIIRPOP 111
Db 62 NLRHAKHLIVERQPMFATSDYSSWARPTVGLKRTFCP---RPPP 103

RESULT 8
Q6X247 PRELIMINARY; PRT; 125 AA.
AC Q6X247;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE UL35 capsid protein.
GN ORFNames=BHV5-21;
OS Bovine herpesvirus 5.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=35244;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=SV507/99;
RX MEDLINE=22850801; PubMed=12970418;
RX DOI=10.1128/JVI.77.19.10339-10347.2003;
RA Delbon G., Moraes M.P., Lu Z., Afonso C.L., Flores E.F., Weiblen R.,
RA Kutish G.F., Rock D.L.;
RT "Genome of bovine herpesvirus 5.";
RL J. Virol. 77:10339-10347(2003).
DR EMBL; AY261359; AAR86126.1; -.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR InterPro; IPR007584; UL35.
DR Pfam; PF04496; Herpes UL35; 1.
SQ SEQUENCE 125 AA; 13525 MW; BC5634AF35F5289F CRC64;

Query Match 14.3%; Score 173; DB 2; Length 125;
Best Local Similarity 37.3%; Pred. No. 0.0029;
Matches 41; Conservative 17; Mismatches 46; Indels 6; Gaps 3;

QY 1 MTQPASRVVFDPSNPTTFSVEAIAAYTPVALIRLN-ASGFLQPGHRVD-TADARSITYT 58
DB 1 MSAPAG-----IDPSAPATTITPTLRDLFPVLHLVNAASRLQDGTTPQVSAARRNLL 56

QY 59 VGAASAARARANHNANTIRRTAMPAETDPTWLRPTVGLKRTFNRIIR 108
DB 57 VGTSLAMVDLRRRHAKAVPRVPMFATYDHAHWARTIGLKRTFLPRVQ 106

RESULT 9
ID Q39267 PRELIMINARY; PRT; 119 AA.
AC Q39267;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 25.
OS Equid herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10331;
RN [1]_SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RX MEDLINE=98264497; PubMed=9603335;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-4.";
RL J. Gen. Virol. 79:1197-1203(1998).
DR EMBL; AF030027; AAC59540.1; -.
DR PIR; T42568; T42568.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR InterPro; IPR007584; UL35.
DR Pfam; PF04496; Herpes UL35; 1.
SQ SEQUENCE 119 AA; 13667 MW; CC6B4FDD70E2E55E CRC64;

Query Match 12.8%; Score 154.5; DB 2; Length 119;
Best Local Similarity 32.8%; Pred. No. 0.034;
Matches 38; Conservative 12; Mismatches 39; Indels 27; Gaps 3;

QY 9 VVFDPSNPTTFSVEAIAAYTPVALIRLNASGFLQPGHRVDIADARSITYT----- 58
DB 12 VAFDPWDPTNKAANKFMDLPVDVMTILN-----QNIDELD----YTKYSDDEINEG 59

QY 59 -----VGAASAARARANHNANTIRRTAMPAETDPTWLRPTVGLKRTFNRIIR 109
DB 60 LKQLFNGTAKTWVVLQRHLKALVRSAMPAHNDASTWARPNIGLKRTTTPPRFMQP 115

us-09-874-140-2.rup

RESULT 10
VP26_EHV1B
ID VP26_EHV1B STANDARD; PRT; 119 AA.
AC P28974;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Capsid protein VP26.
GN Name=25;
OS Equine herpesvirus 1 (strain Ab4p) (EHV-1) (Equine abortion virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31520;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=92295566; PubMed=1318606;
RX Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1.";
RL Virology 189:304-316(1992).
CC -!- SIMILARITY: Belongs to the herpesviruses UL35 family.

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EMBL; M86664; AAB02460.1; -.
DR PIR; H36797; WZBBB7.
DR InterPro; IPR007584; UL35.
DR Pfam; PF04496; Herpes_UL35; 1.
KW Coat protein.
SQ SEQUENCE 119 AA; 13596 MW; 3603A1AA4208CB08 CRC64;

Query Match 12.7%; Score 153.5; DB 1; Length 119;
Best Local Similarity 31.1%; Pred. No. 0.039;
Matches 37; Conservative 16; Mismatches 45; Indels 21; Gaps 3;

QY 3 QPASSRVVFDPSNPTTFSVEAIAAYTPVALIRLNASGFLQPGHRVDIADARSITYT---- 58
DB 6 QQQQAPVAFNPADPNKAAKFMDLPVDVITILN-----QNIDELDYTK-VTEDEI 56

QY 59 -----VGAASAARARANHNANTIRRTAMPAETDPTWLRPTVGLKRTFNRIIR 109
DB 57 SEGLKQLFMGTARTWVSLRQRHLKSLVRRSDMPAQNDASTWARPNIGLKRTTTPPRFMQP 115

RESULT 11
Q6S6P6
ID Q6S6P6 PRELIMINARY; PRT; 119 AA.
AC Q6S6P6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Capsid protein.
OS Equid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10326;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=V592;
RX Davis-Poynter N.J., Nugent J., Birch-Machin I., Allen G.P.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Ab4;
RC MEDLINE=92295566; PubMed=1318606;
RX Telford E.A., Watson M.S., McBride K., Davison A.J.;
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RT "The DNA sequence of equine herpesvirus-1.";  
RL Virology 189:304-316(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ab4;  
RA Davison A.J.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY464052; AAS45909.1; -;  
DR EMBL; AY665713; AAT67282.1; -;  
DR GO; GO:0019028; C:Viral capsid; IEA.  
DR InterPro; IPR007584; UL35.  
DR Pfam; PF04496; Herpes UL35; 1.  
SQ SEQUENCE 119 AA; 13596 MW; 3603A1AA208CB08 CRC64;  
  
Query Match 12.7%; Score 153.5; DB 2; Length 119;  
Best Local Similarity 31.1%; Pred. No. 0.039;  
Matches 37; Conservative 16; Mismatches 45; Indels 21; Gaps 3;  
  
QY 3 QPASRVVDFSNPTTFSVEIAAYTPVALITLLNASGLPQGHVDTADARSYIT----- 58  
DB 6 QQQAPVAFNPADPPNKAANFKDMLPVDVITIL-----QNIDELDYTK-YTEDEI 56  
  
QY 59 -----VGAASAARARAHNANTIRRTAMFAETDPMWLRPTVGLKRTFNPIIRP 109  
DB 57 SEGLKQLFMGTARTVSLRQHLKSLVRSDMFANDASTWARPNIGLKRTFPFRFMQP 115  
  
RESULT 12  
Q66IV2 PRELIMINARY; PRT; 503 AA.  
ID Q66IV2  
AC TISSUE=Eye;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE MGC84356 protein.  
GN Name=MGC84356;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RA Klein S., Gerhard D.S.;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
CC 1- SIMILARITY: Contains 1 SH3 domain.  
DR EMBL; BC081178; AAB81178.1; -;  
DR InterPro; IPR00108; Neu_cyt_fact_2.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR011511; SH3 2.  
DR InterPro; IPR000727; T_SNARE.  
DR Pfam; PF00018; SH3_1; 1.  
DR Pfam; PF07653; SH3_2; 1.  
DR PRINTS; PR00499; P67PHOX.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS00002; SH3; 1.  
DR PROSITE; PS50192; T_SNARE; 1.  
KW SH3 domain.  
SQ SEQUENCE 503 AA; 54100 MW; DED356AEB64A2C09 CRC64;  
  
Query Match 11.8%; Score 142; DB 2; Length 503;  
Best Local Similarity 29.9%; Pred. No. 0.79;  
Matches 53; Conservative 20; Mismatches 68; Indels 36; Gaps 10;  
  
QY 69 RANHNANTIRRTAMFAETDPMWLRPTVGLKRTFNPIIRPQPPNPM-SLIGSP--TI 125  
DB 157 KAHGGNQARTGLTRTNPT-QKP-----PSPMPSPRGLGRNTPYKTL 201  
  
QY 126 LPQKTSADQSALQOPALAFSSQHPPTTSASVGQOQHVVGSS-GQQPQGGQAS 184  
DB 202 EPVKPPTVPNDYMTSPARL---GS--QHSQPT--ASLNQRPRTSHSGSGSGSRENSGS 254  
  
QY 185 STV-----QPTTGSPPAQGV-----POSTPPTQNTPQGGQTLSTHTGSGNASR 231  
DB 255 SSIGIPAVPTSPPTVQGGISGGPPPPPPPPPPPPPPPPVPGTGSAPASQFGSMTR 311  
  
RESULT 13  
Q76N76 PRELIMINARY; PRT; 771 AA.  
ID Q76N76  
AC TISSUE=Wistar;  
RX MEDLINE=99013250; PubMed=9798906;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE GEP-1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wistar;  
RX PubMed=99013250; PubMed=9798906;  
RA Ogura K., Kohno K., Tai T.;  
RT "Molecular cloning of a rat brain cDNA, with homology to a tyrosine  
kinase substrate, that induces galactosylceramide expression in COS-7  
cells.";  
RL J. Neurochem. 71:1827-1836(1998).  
DR EMBL; AB002811; BAD08342.1; -;  
DR HSSP; Q9UUY5; 1JWG.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0006886; P:intracellular protein transport; IEA.  
DR InterPro; IPR008942; ENTH_VHS.  
DR InterPro; IPR011011; FYVE_PHD_znf.  
DR InterPro; IPR003903; UIM.  
DR InterPro; IPR002014; VHS.  
DR InterPro; IPR000306; Znf_FYVE.  
DR Pfam; PF01363; FYVE; 1.  
DR Pfam; PF02809; UIM; 1.  
DR Pfam; PF00790; VHS; 1.
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DR ProDom; PD003686; VHS; 1.
DR SMART; SM00064; FYVE; 1.
DR SMART; SM00288; VHS; 1.
DR PROSITE; PS03030; UIM; 1.
DR PROSITE; PS0179; VHS; 1.
DR PROSITE; PS0178; ZF_FYVE; 1.
SQ SEQUENCE 771 AA; 8578 MW; 4A0DFA0A58176739 CRC64;

Query Match 11.7%; Score 141.5; DB 2; Length 771;
Best Local Similarity 28.2%; Pred.No.1.3; Mismatches 61; Indels 14;
Matches 67; Conservative 24;

QY 4 PASSRVVFPSPNPTTF-----SVEAIAATYTPVALIRLLNASGPL--QPGRHVDIADA 53
DB PTAGGVLYQPSGPTSPGTFSPAGSVGSPMH-GVTMSQAPATGYPYPMPTAD-PSM 630
QY 54 RSIYTVGAASARARANINANTIRRTAMFAETDPTWLRPTVGLKRTNPIIRPOP-P 112
DB STRAINT=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
QY 113 NPSMSLIGISGPTLPKQTSADQSAL---QPAALAFSGSSPQHPPPTT---SASVG 164
DB 667 TP-----GYAPQSLPAISQPPQTSNIGYMSQPMGYPYMNQ--LMTILPGQDASLP 720
QY 165 QQQHVVGSSGQQPQQGASSTVQPTTGSPPAAQGVPOSTPTPTQNTP-QGKGQTL 221
DB 721 AQOPYI---TGQPMYQQMAPSTGPPQPPVAQ-----PPPTGPPAQNQTQLIS 769

RESULT 14
Q6P9L3 PRELIMINARY; PRT; 1114 AA.
AC Q6P9L3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Falz protein.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalaia U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC060715; AH060715.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00439; Bromodomain; 1.
DR Pfam; PF00628; PHD; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS00633; BROMODOMAIN_1; 1.
DR PROSITE; PS00014; BROMODOMAIN_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
SQ SEQUENCE 1114 AA; 121422 MW; 7A3906159D59599B CRC64;

Query Match 11.5%; Score 139; DB 2; Length 1114;
Best Local Similarity 27.0%; Pred.No.2.7; Mismatches 54; Gaps 9;
Matches 57; Conservative 23;

QY 54 RSIYT-VGAASARARANINANTIRRTAMFA-----ETDPMWLRPTVGLKR 100
DB 413 RFLFTPLSTSAFASSSSNSTTTNATAAGSGEQKSKILPQTQVQPATTLAPT--QSS 470
QY 101 TNPRIIPQPPNPSLIGSGPTLPKQTSADQSALQOPPAALAFSGSSPQHPPPTTS 160
DB 471 SVSPAEPQPAQPA-----AQFQ--PQPPPAQPEVQTQPAVSVHVPSETQPSQAQTSK 523
QY 161 ASVG---QQQHVVGSS-----GQPPQQAQASSTVQPTTGSPP 195
DB 524 PLVATQCPQSSVQGSQSPRVQSPPLTRIRPSTPQVTFGQQPQ--VQTASQPIPIPP 581
QY 196 A-----AQGVPOSTPPTQNTPQGGKQTL 221
DB 582 TSLQAPSGQPSQPSQVQSSTQTLSSGQTLN 612

RESULT 15
Q9UJ50 PRELIMINARY; PRT; 776 AA.
AC Q9UJ50;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hrs.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20286537; PubMed=10825299;
RA Kwong J., Roudabush F.L., Moore P.H., Montague M., Oldham W., Li Y.,
RA Chin L.-S., Li L.;
RT "Hrs interacts with SNAP-25 and regulates Ca2+-dependent exocytosis.";
RL J. Cell Sci. 113:2273-2284(2000).
DR HMBL; AF036344; AAF76251.1; -.
DR HSSP; O960X8; LDVP.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0008886; P:intracellular protein transport; IEA.
DR InterPro; IPR008942; ENTH_VHS.
DR InterPro; IPR011011; FYVE_PHD_Znf.
DR InterPro; IPR003903; UIM.
DR InterPro; IPR002014; VHS.
DR InterPro; IPR000306; Znf_FYVE.
DR Pfam; PF01363; FYVE; 1.
DR Pfam; PF02809; UIM; 1.
DR Pfam; PF00790; VHS; 1.
DR ProDom; PD003686; VHS; 1.
DR SMART; SM00064; FYVE; 1.
DR SMART; SM00726; UIM; 1.
DR SMART; SM00288; VHS; 1.
DR PROSITE; PS00330; UIM; 1.
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DR PROSITE; PS50179; VHS; 1.
DR PROSITE; PS50178; 2F_PXVE; 1.
SQ SEQUENCE 776 AA; 86246 MW; FD61BEC121F37E67 CRC64;

Query Match
Best Local Similarity 27.6%; Pred. No. 2.1;
Matches 66; Conservative 26; Mismatches 89; Indels 58; Gaps 14;

Qy 4 PASSRVVFDPSNPITP-----SVEAIAAYTVVALIRLLNAGSL--QGRHVRDITADA 53
Db 573 PTAGGVLYQSGPTSFCTTSPAGSVGSGPMH-GVYMSQPAPATGVPSMPTTAD-PSM 630

Qy 54 RSIYTVGAASAARARANHNANTIRTAMFAETDPTMTWLRPTVGLKRTFNRIIRPO-P 112
Db 631 VSAIYWPAGAPGAQA-----APQAQAGFTT-----NPAYSSYQPTP 666

Qy 113 NPS-MSIIGISGPTLLPKQTSADQSAI-----QQPAALAFSGSSPQHPPQPTT-----SASV 163
Db 667 TPGYQNVASQAPQSLPAISLPQPTNTGYMGSQPMWMCYQYNNQN-----LMTTLPGQDASL 724

Qy 164 GQQQHVVGSSGQQPQQGAQSSVTQPTTGSPPAAQGVPPQSTPTPTQNTP-QGKGQTLIS 221
Db 725 PAQOPYI---TGQQPMYQOMAPSTGPPQQQPPVAQ-----PPPTQGPAPAGNQTQLIS 774

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Search completed: September 25, 2005, 21:01:59
Job time : 391 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 25, 2005, 20:26:05 ; Search time 119 Seconds
(without alignments)
147.416 Million cell updates/sec

Title: US-09-874-140-2
Perfect score: 1206
Sequence: 1 MTQPASSRVFDPSPNPTTFS.....KGQTLSTHTGSGNASRRRV 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/1aa/5A COMB.pap:*
 - 2: /cgn2_6/ptodata/1/1aa/5B COMB.pap:*
 - 3: /cgn2_6/ptodata/1/1aa/6A COMB.pap:*
 - 4: /cgn2_6/ptodata/1/1aa/6B COMB.pap:*
 - 5: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pap:*
 - 6: /cgn2_6/ptodata/1/1aa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	235	3	US-09-219-337-2
2	128.5	10.7	480	3	US-09-189-035-5
3	128.5	10.7	480	3	US-09-382-086-5
4	127.5	10.6	531	4	US-09-949-016-8074
5	127.5	10.6	907	3	US-08-783-774-2
6	127.5	10.6	907	4	US-09-328-599A-1
7	127.5	10.6	907	5	PCT-US95-04611A-19
8	123	10.2	276	4	US-09-538-092-889
9	123	10.2	331	4	US-09-538-092-845
10	123	10.2	529	4	US-09-949-016-11657
11	122	10.1	2441	1	US-08-194-468-2
12	122	10.1	2441	3	US-08-961-739-2
13	122	10.1	2441	3	US-09-514-247A-8
14	122	10.1	2441	4	US-09-686-316-2
15	121.5	10.1	258	4	US-09-949-016-9409
16	121	10.0	251	4	US-09-538-092-840
17	120.5	10.0	234	4	US-09-538-092-888
18	120	10.0	677	1	US-08-188-582-13
19	120	10.0	677	1	US-08-646-715-13
20	120	10.0	677	4	US-09-538-092-1164
21	120	10.0	694	4	US-09-949-016-8775
22	120	10.0	694	4	US-09-949-016-8775
23	120	10.0	711	4	US-09-949-016-8493
24	119	9.9	258	4	US-09-248-796A-23723
25	119	9.9	320	4	US-09-252-991A-21056
26	118.5	9.8	247	4	US-09-538-092-880
27	118.5	9.8	542	4	US-09-538-092-289

28	118	9.8	878	4	US-09-556-706B-2	Sequence 2, Appli
29	118	9.8	878	4	US-09-724-418A-2	Sequence 2, Appli
30	118	9.8	1109	4	US-09-949-016-10771	Sequence 10771, A
31	118	9.8	1203	4	US-09-949-016-6615	Sequence 6615, Ap
32	117	9.7	577	4	US-10-029-180-48	Sequence 48, Appl
33	117	9.7	2442	3	US-09-514-247A-10	Sequence 10, Appl
34	117	9.7	2442	4	US-09-538-092-1370	Sequence 1370, Ap
35	115.5	9.6	124	2	US-08-925-237-2	Sequence 2, Appli
36	115	9.5	419	4	US-09-248-796A-21670	Sequence 21670, A
37	115	9.5	666	4	US-09-050-739-70	Sequence 70, Appl
38	114.5	9.5	320	4	US-09-949-016-8196	Sequence 8196, Ap
39	114.5	9.5	593	4	US-09-252-991A-17983	Sequence 17983, A
40	113	9.4	662	4	US-09-902-540-12594	Sequence 12594, A
41	113	9.4	696	3	US-08-906-885-4	Sequence 4, Appli
42	113	9.4	696	3	US-09-129-668-4	Sequence 4, Appli
43	113	9.4	705	4	US-09-538-092-945	Sequence 945, App
44	113	9.4	713	4	US-09-949-016-9700	Sequence 9700, Ap
45	113	9.4	776	4	US-09-266-225D-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-219-337-2
; Sequence 2, Application US/09219337
; Patent No. 6258363
; GENERAL INFORMATION:
; APPLICANT: EICKMANN, Markus
; APPLICANT: GICKLHORN, Dorothee
; APPLICANT: RAUSAK, Klaus
; APPLICANT: HAUSER, Hans-Peter
; APPLICANT: GIESENDOERF, Bernhard
; TITLE OF INVENTION: VARICELLA ZOSTER VIRUS (VZV) IMMUNOREACTIVE PROTEIN
; FILE OF INVENTION: VP26 AND ITS DIAGNOSTIC USE
; FILE REFERENCE: 058315/0127
; CURRENT APPLICATION NUMBER: US/09/219,337
; CURRENT FILING DATE: 1998-12-23
; EARLIER APPLICATION NUMBER: DE 197 57 765.2
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Varicella Zoster Virus
US-09-219-337-2

Query Match	100.0%	Score 1206;	DB 3;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 1.3e-93;		
Matches 235;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	
Qy	1	MTQPASSRVFDPSPNPTTFSVEAIAATPVALIRLLNAGSLPQGHRYVDIADARSIIYTVG	60	
Db	1	MTQPASSRVFDPSPNPTTFSVEAIAATPVALIRLLNAGSLPQGHRYVDIADARSIIYTVG	60	
Qy	61	AAASAARARAHNANTIRRTAMFAETDPMTWLRTVGLKRTFNPRRIIRPQPPNPSMSLGI	120	
Db	61	AAASAARARAHNANTIRRTAMFAETDPMTWLRTVGLKRTFNPRRIIRPQPPNPSMSLGI	120	
Qy	121	SGPTLPKQTSADQSAALQPPAALAFSGSSPHPPQTTSASVGGQOHVVGSSSQQQPQQ	180	
Db	121	SGPTLPKQTSADQSAALQPPAALAFSGSSPHPPQTTSASVGGQOHVVGSSSQQQPQQ	180	
Qy	181	GAQSTVQPTTGSPPAAQGVFQSTPPPTQNTPOGKGQTLSTHTGSGNASRRRV	235	
Db	181	GAQSTVQPTTGSPPAAQGVFQSTPPPTQNTPOGKGQTLSTHTGSGNASRRRV	235	

RESULT 2
US-09-189-035-5
; Sequence 5, Application US/09189035
; Patent No. 6020165

```

; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
; FILE REFERENCE: PF-0638 US
; CURRENT APPLICATION NUMBER: US/09/189,035
; CURRENT FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: g2245671
; US-09-189-035-5

Query Match 10.7%; Score 128.5; DB 3; Length 480;
Best Local Similarity 28.2%; Pred. No. 0.0067;
Matches 51; Conservative 17; Mismatches 66; Indels 47; Gaps 8;

QY 69 RANHNANTIRRTAMFAETDPMTWLRPTVGLKRTFNRIIRPQPPNPSMS-----LGISGP- 123
Db 157 KAKHGNQPARTGTLRTPPT-----QKPPSPPMGSGRGTGRLGRNTPY 198

QY 124 -TILPQKTSADQSALQQAALAFSGSSPQHPPTTSASVGGQOHV-VSGSSGQPPQOG 181
Db 199 KTLPEVKPPTVPNDYMTSPARL---GS--QHSPGRTASLNQRPRTTHSGSGSGSRENSG 253

QY 182 AQS--STVQPTTGSPPAAQGVPOSTP-----PPTQNTPOGKGOTLSHTG 224
Db 254 SSSIGIPIAVPTSPPTIGPAPGSAQSGYGTMTTRQISRHNSTTSSTSGGYRRTPSVTA 313

QY 225 Q 225
Db 314 Q 314

RESULT 4
US-09-949-016-8074
; Sequence 8074, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8074
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8074

Query Match 10.6%; Score 127.5; DB 4; Length 531;
Best Local Similarity 26.0%; Pred. No. 0.0092;
Matches 54; Conservative 18; Mismatches 57; Indels 79; Gaps 9;

QY 72 HNANTIRRTAMFAETDPMTWLRPTVGLKRTFNRIIRPQPPNPSMS-----LGISGP--TI 125
Db 183 HGNQPARTGTLRTPPT-----QKPPSPPMGSGRGTGRLGRNTPYKTL 224

QY 126 LPQKTSADQSALQQAALAFSGSSPQHPPTTSASVGGQOHV-VSGSSG----- 175
Db 225 EFKPPTVPNDYMTSPARL---GS--QHSPGRT--ASLNQRPRTTHSGSGSGSRENSG 277

QY 176 -----QKPPSPPMGSGRGTGRLGRNTPYKTL 205
Db 278 SSSIGIPIAVPTSPPTIGPAPGSAQSGYGTMTTRQISRHNSTTSSTSGGYRRTPSVTA 337

QY 206 -----PPTQNTPOGKGOTLSHTG 225
Db 338 TRQISRHNSTTSSTSGGYRRTPSVTAQ 365

RESULT 5
US-08-783-774-2
; Sequence 2, Application US/08783774
; Patent No. 6054130
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Jackman, Winthrop
; TITLE OF INVENTION: NON-SPLICING VARIANTS OF
; GP350/220
; NUMBER OF SEQUENCE: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

```

; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/783,774
; FILING DATE: 15-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 907 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-783-774-2

Query Match 10.6%; Score 127.5; DB 3; Length 907;
Best Local Similarity 24.9%; Pred. No. 0.018;
Matches 64; Conservative 26; Mismatches 88; Indels 79; Gaps 14;

OY 2 TOPASSRVVFD--SNPT---TFSVEAIAAATPVVALIRLLNASGPLQPGHVRVDIADARSI 56
Db 577 TSPTSATVTPPNATSPILGKTSPTSATVTPP-----NATGP----- 614

OY 57 YTVGAASAARARAHNANTIRRTAMFAETDPMTWLRTVGLKRTFNRIIRPQPNPSM 116
Db 615 -TVGETSPQANA-TNH---TLGGTS-----PT-----PVVTSQPKNATS 648

OY 117 SLGISGPTLPKQTQSDQSALQOPAL--AFSGSSPOHPP-----PQTSA 161
Db 649 AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTDNSTSHMPLLTSAHPTGGENITQVTPA 708

OY 162 SVGQQQHVVGSSGQOQQAQSTVQP---TTGSPAAQGVPOSTPPPTQNTPOGKGQ 218
Db 709 SI--STHVSTSS-PEPRGTTSSQASGCGNSSTSKPGEVNVTKGTPPNATSPQAPSGQ 765

OY 219 -----TLSHTGSGNAS 230
Db 766 KTAVPTVTSTGKANST 782

RESULT 6
US-09-328-599A-1
; Sequence 1, Application US/09328599A
; Patent No. 6432679
; GENERAL INFORMATION:
; APPLICANT: MOND, James J. and Lees, Andrew
; TITLE OF INVENTION: Enhancement of B Cell Activation by
; TITLE OF INVENTION: Co-Ligation of Receptors for Antigen and Complement C3d
; TITLE OF INVENTION: Using EBV gp350/220 or EBV gp350/220 Peptide Adjuvants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,599A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B.
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 04995.6025-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 907 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-328-599A-1

Query Match 10.6%; Score 127.5; DB 4; Length 907;
Best Local Similarity 24.9%; Pred. No. 0.018;
Matches 64; Conservative 26; Mismatches 88; Indels 79; Gaps 14;

OY 2 TOPASSRVVFD--SNPT---TFSVEAIAAATPVVALIRLLNASGPLQPGHVRVDIADARSI 56
Db 577 TSPTSATVTPPNATSPILGKTSPTSATVTPP-----NATGP----- 614

OY 57 YTVGAASAARARAHNANTIRRTAMFAETDPMTWLRTVGLKRTFNRIIRPQPNPSM 116
Db 615 -TVGETSPQANA-TNH---TLGGTS-----PT-----PVVTSQPKNATS 648

OY 117 SLGISGPTLPKQTQSDQSALQOPAL--AFSGSSPOHPP-----PQTSA 161
Db 649 AVTTGQHNTSSSTSSMSLRPSSNPETLSPSTDNSTSHMPLLTSAHPTGGENITQVTPA 708

OY 162 SVGQQQHVVGSSGQOQQAQSTVQP---TTGSPAAQGVPOSTPPPTQNTPOGKGQ 218
Db 709 SI--STHVSTSS-PEPRGTTSSQASGCGNSSTSKPGEVNVTKGTPPNATSPQAPSGQ 765

OY 219 -----TLSHTGSGNAS 230
Db 766 KTAVPTVTSTGKANST 782

RESULT 7
PCT-US95-04611A-19
; Sequence 19, Application PC/TUS9504611A
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard and Jackman, Winthrop, T.
; TITLE OF INVENTION: Non Splicing Variants of gp350/220
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04611A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: 08/229,291
/ FILING DATE: April 18, 1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Luann Cseri
/   REGISTRATION NUMBER: 31,822
/   REFERENCE/DOCKET NUMBER: AVIR-003/00US
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 415-843-5163
/   TELEFAX: 415-857-0663
/   TELEX: 380816 CooleyPA
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 907 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/ MOLECULE TYPE: protein
PCT-US95-04611A-19

Query Match      10.6%; Score 127.5; DB 5; Length 907;
Best Local Similarity 24.9%; Pred. No. 0.018;
Matches 64; Conservative 26; Mismatches 88; Indels 79; Gaps 14;

QY 2 TOPASSRVVDP--SNPT---TFSVEAIAAYTPVALIRLLNAGSLQPGHRVDIADARS1 56
Db 577 TSPTSAVTTPTNATSTPLTKTSPTSASTTPTP-----NATGP----- 614
QY 57 YTVGAASARARANNANIRTAMFAETDPMTWLRPTVGLKRTFNPIIRPQPNPSM 116
Db 615 -TVGETSPQANA-TNH---TLGGS-----PT-----PVTSPQKNATS 648
QY 117 SLGISGPTILPQKTSADQSALQOAPAL--AFSGSSPQHPP-----POTTS 161
Db 649 AVTTGQHNITSSSTSMRLSPSNPTLSFSDNSTSHMPLTSAHPTGGENITQVTP 708
QY 162 SVGQQQHVWVGSGGQQPQQAQSSVTQP---TTGSPPAAGVVPQSTPTPTNTPOGKG 218
Db 709 SI--STHHVSTSS-PEPRPTTSQASGPGNSSTSTKPGVNVTKGTPPNQATSPQAPS 765
QY 219 -----TLSHTGQSGNAS 230
Db 766 KTAIVPTVTSTGKANST 782

RESULT 8
US-09-538-092-889
; Sequence 889, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538, 092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 889
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P10162
US-09-538-092-889

Query Match      10.2%; Score 123; DB 4; Length 276;
Best Local Similarity 32.1%; Pred. No. 0.0099;
Matches 44; Conservative 7; Mismatches 59; Indels 26; Gaps 6;

QY 108 RQPPNPSMSLIGISGPTILPQKTSADQSALQOAPALAFSGSSPQHPPQ-----TTSAS 162
Db 157 KPQGGPPQGGNQPGPPPPPPPGKPGPQGGNRPGGPPPG--KPQGGPPPGDKSRSPSP 215
QY 163 VQQQQHVWVGSGGQQPQQAQSSVTQPTTGTSPPAAGVVPQSTPTPTNTPOG---GKQ 218
Db 216 PKPQ-----GPPPGQGNQ-----GPPPPPGKPGPQGGNRPGGPPPGKPG 261
QY 219 TLSHTGQSGNASR 234
Db 262 --GPPAQGGSKSQSAR 275

RESULT 9
US-09-538-092-845
; Sequence 845, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538, 092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 845
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P04280
US-09-538-092-845

Query Match      10.2%; Score 123; DB 4; Length 331;
Best Local Similarity 32.4%; Pred. No. 0.012;
Matches 44; Conservative 7; Mismatches 59; Indels 26; Gaps 6;

QY 108 RQPPNPSMSLIGISGPTILPQKTSADQSALQOAPALAFSGSSPQHPPQ-----TTSAS 162
Db 157 KPQGGPPQGGNQPGPPPPPPPGKPGPQGGNRPGGPPPG--KPQGGPPPGDKSRSPSP 215
QY 163 VQQQQHVWVGSGGQQPQQAQSSVTQPTTGTSPPAAGVVPQSTPTPTNTPOG---GKQ 218
Db 216 PKPQ-----GPPPGQGNQ-----GPPPPPGKPGPQGGNRPGGPPPGKPG 261
QY 219 TLSHTGQSGNASR 234
Db 262 --GPPAQGGSKSQSAR 275

RESULT 10
US-09-949-016-11657
; Sequence 11657, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11657
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11657

Query Match
Best Local Similarity 10.2%; Score 123; DB 4; Length 529;
Matches 60; Conservative 24; Mismatches 105; Indels 26; Gaps 9;

QY 13 PGNPTTFSVEAIAATVPVALIRLLNASGLOPCHRVDIADARSITYTVGAAASAARARANH 72
Db 227 PTAPSVFS--PTGNRTPIPPSRTL-----LRKRGVKLLDISELDWVGAGREKRRKTL 279
QY 73 NANTIRRTAMFAETDPMTWLRP--TVGLKRTFNPRRIIPQPNPNSMLGISGPTILPOKT 130
Db 280 DAEVVEKPA--KEETVVENATPDYAAGLVSTQKLGSLNNEPALPSTSYLPSTPSVVP--A 335
QY 131 QSADOSALQOAPALAFSGSSPOHPP--PQTTSASVGOQHV--SGSSGOQPOQGAQSS- 185
Db 336 SSYIPSETPPAPSGREASRPPEEPSAPSTLPAQFKQKAPMNSGLSPATPTPAAPTSP 395
QY 186 -----TVQPTTGGPPAAQGVPPQSTPPTQNTQP 213
Db 396 LPTTPPAVAPTQTPPVAVAPQ--TOAPAQQPK 429

RESULT 11
US-08-194-468-2
; Sequence 2, Application US/08194468
; Patent No. 5750336
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
; TITLE OF INVENTION: RESPONSIVE GENES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,468
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)-546-4737
; TELEFAX: (619)-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-194-468-2

us-09-874-140-2.ra1

Query Match
Best Local Similarity 10.1%; Score 122; DB 1; Length 2441;
Matches 81; Conservative 24; Mismatches 103; Indels 94; Gaps 18;

QY 4 PASSRVVFDPSNPTTFSV-----EATAAATPVALIRLLNASGLOP-----GHRVDIA 51
Db 696 PAQS--VRPPNGPLPLPVNRMOVSGQGNMNFPMISLGNVQLPQAPMGPRASPMHSHVQMN 753
QY 52 DARSITYTVGAAASAARARANH-----ANTIRRTAMFAETDPMTWLRPTVGLKRTFNPRI 106
Db 754 SMAVS--PGMAISPRMPQPPNMMGTHANNMAQA-----PT-----QNQ 791
QY 107 IRQPQNPMSLIGISGPTI-LPQKTSADQALQOPAA-----LAFSGS----- 149
Db 792 FLQNPQPFSSGAMSVNSVGMGPAAQAGVSGQEPGAALPNLMLAPQASQLPCPPVT 851
QY 150 -SPOH--PPQPTTSASVGOQHV--VVGSSGOQPOQGAQSS-----TVQPTTGGPPAA- 197
Db 852 QSPHLPTPPASTAAGMPSLQHPAPGWTTPQPAAPTQSTPVSSGQPTTPTPGSVPSAA 911
QY 198 --QGVV-----QSTP-----PPTQNTPOGKGO--TLSHTGQSGN-----ASRSR 233
Db 912 QTQSTPTVQAAQAQVTPQPTPVQPPSVATPQSSQQQPTPVHTQPPGTPPLSQAASIDN 971
QY 234 RV 235
Db 972 RV 973

RESULT 12
US-08-961-739-2
; Sequence 2, Application US/08961739A
; Patent No. 6063583
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
; FILE REFERENCE: SALK1650-1
; CURRENT APPLICATION NUMBER: US/08/961,739A
; CURRENT FILING DATE: 1997-10-31
; EARLIER APPLICATION NUMBER: US 194,468
; EARLIER FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2441
; TYPE: PRT
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2441)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-08-961-739-2

Query Match
Best Local Similarity 10.1%; Score 122; DB 3; Length 2441;
Matches 81; Conservative 24; Mismatches 103; Indels 94; Gaps 18;

QY 4 PASSRVVFDPSNPTTFSV-----EATAAATPVALIRLLNASGLOP-----GHRVDIA 51
Db 696 PAQS--VRPPNGPLPLPVNRMOVSGQGNMNFPMISLGNVQLPQAPMGPRASPMHSHVQMN 753
QY 52 DARSITYTVGAAASAARARANH-----ANTIRRTAMFAETDPMTWLRPTVGLKRTFNPRI 106
Db 754 SMAVS--PGMAISPRMPQPPNMMGTHANNMAQA-----PT-----QNQ 791
QY 107 IRQPQNPMSLIGISGPTI-LPQKTSADQALQOPAA-----LAFSGS----- 149
Db 792 FLQNPQPFSSGAMSVNSVGMGPAAQAGVSGQEPGAALPNLMLAPQASQLPCPPVT 851
QY 150 -SPOH--PPQPTTSASVGOQHV--VVGSSGOQPOQGAQSS-----TVQPTTGGPPAA- 197
Db 852 QSPHLPTPPASTAAGMPSLQHPAPGWTTPQPAAPTQSTPVSSGQPTTPTPGSVPSAA 911
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QY 198 --QGVF-----QSTP-----PPTQNTPGGKGQ-TLSHTGSGN-----ASRSR 233
Db 912 QTGSTTVQAAAQAQVTPQPTVPQPPSVATPQSSQQPTPVHTQPGTPLSQAAASIDN 971
QY 234 RV 235
Db 972 RV 973

RESULT 13

US-09-514-247A-8
; Sequence 8, Application US/09514247A
; Patent No. 6365361
; GENERAL INFORMATION:
; APPLICANT: TANABE SEIYAKU CO. LTD.
; APPLICANT: TANIGUCHI, Tomoyasu
; APPLICANT: MIZUKAMI, Junko
; TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPA
; FILE REFERENCE: TANIGUCHI=6
; CURRENT APPLICATION NUMBER: US/09/514,247A
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT/JP98/03734
; PRIOR FILING DATE: 1998-08-24
; PRIOR APPLICATION NUMBER: JP231084/1997
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 2441
; TYPE: PRT
; ORGANISM: mouse
US-09-514-247A-8

Query Match 10.1%; Score 122; DB 3; Length 2441;
Best Local Similarity 26.8%; Pred. No. 0.17;
Matches 81; Conservative 24; Mismatches 103; Indels 94; Gaps 18;

QY 4 PASSRVVFDPSNPTTFVS-----EAIAYTPVALIRLLNASGLOP-----GHRVDIA 51
Db 696 PAQS--VRPENGPLPLPVNRMQVSGMNSFPMSLGNVQLPQAPMGPRAAASPMNHSVQVN 753
QY 52 DARSIVTVGAAASAAARANHN-----ANTIRTFAMFAETDPTWLRPTVGLKRTFNPRI 106
Db 754 SMAVS--PGMAISPSRMPQPPNMGMTHANNIMAQA-----PT-----QNG 791
QY 107 IRPQPNPNSLSIGSPTI-LPQKTSADQSALQOPAA-----LAFSGS-----149
Db 792 FLQNFQFPSSSGMNSVSGMGQPAQAQVSGQGPAGALPNPLNMLAFQASQLPCPPVT 851
QY 150 -SPQH--PPQTTASVGGQOH-VVSGSGQQPQGAQSS-----TVQPTTGSPPAA- 197
Db 852 QSLPHTPPASTAAGMPSLQHTAPGWTTPQPAAPTQSTPVSSGQTPTPTPGSVPSAA 911
QY 198 --QGVF-----QSTP-----PPTQNTPGGKGQ-TLSHTGSGN-----ASRSR 233
Db 912 QTGSTTVQAAAQAQVTPQPTVPQPPSVATPQSSQQPTPVHTQPGTPLSQAAASIDN 971
QY 234 RV 235
Db 972 RV 973

RESULT 14

US-09-686-316-2
; Sequence 2, Application US/09686316
; Patent No. 6646115
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
; FILE REFERENCE: SALK1650-1
; CURRENT APPLICATION NUMBER: US/09/686,316
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US/08/961,739

; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 194,468
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2441
; TYPE: PRT
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2441)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-686-316-2

Query Match 10.1%; Score 122; DB 4; Length 2441;

Best Local Similarity 26.8%; Pred. No. 0.17;
Matches 81; Conservative 24; Mismatches 103; Indels 94; Gaps 18;

QY 4 PASSRVVFDPSNPTTFVS-----EAIAYTPVALIRLLNASGLOP-----GHRVDIA 51
Db 696 PAQS--VRPENGPLPLPVNRMQVSGMNSFPMSLGNVQLPQAPMGPRAAASPMNHSVQVN 753
QY 52 DARSIVTVGAAASAAARANHN-----ANTIRTFAMFAETDPTWLRPTVGLKRTFNPRI 106
Db 754 SMAVS--PGMAISPSRMPQPPNMGMTHANNIMAQA-----PT-----QNG 791
QY 107 IRPQPNPNSLSIGSPTI-LPQKTSADQSALQOPAA-----LAFSGS-----149
Db 792 FLQNFQFPSSSGMNSVSGMGQPAQAQVSGQGPAGALPNPLNMLAFQASQLPCPPVT 851
QY 150 -SPQH--PPQTTASVGGQOH-VVSGSGQQPQGAQSS-----TVQPTTGSPPAA- 197
Db 852 QSLPHTPPASTAAGMPSLQHTAPGWTTPQPAAPTQSTPVSSGQTPTPTPGSVPSAA 911
QY 198 --QGVF-----QSTP-----PPTQNTPGGKGQ-TLSHTGSGN-----ASRSR 233
Db 912 QTGSTTVQAAAQAQVTPQPTVPQPPSVATPQSSQQPTPVHTQPGTPLSQAAASIDN 971
QY 234 RV 235
Db 972 RV 973

RESULT 15

US-09-949-016-9409
; Sequence 9409; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9409
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9409

Query Match 10.1%; Score 121.5; DB 4; Length 258;
Best Local Similarity 24.8%; Pred. No. 0.012;
Matches 55; Conservative 16; Mismatches 102; Indels 49; Gaps 8;


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Db 9 SSEMILLISVALLALSSAESSE-----DVSQEEFLISGKPERRPOGGNQFQ---- 59
Qy 80 TAMFAETDPTWLRPTVGLKRTFNPRIIRPOPPNPFMSLSIGSGPTILPQKTSADQSALQ 139
Db 60 -----RPP-----PPGKPGPPPOGGNQSGPPPPPKPEGRPPQGGN 98
Qy 140 QPAALAFSGSSPQHPPPTTSASVQQQHVVSQSGQ----QPQQAQSTVQPTTGSP- 194
Db 99 QSQGPPPHGKPERPPPGQ-----GNQSGTTPPPGKPERPPPOGGNQSHRPPPPGKPE 153
Qy 195 -PAAQGVQST-PPPTQNTPOGKGQTLSHTCQSGNASRSRR 234
Db 154 RPPPOGGNQSGPPPHGKPEG-----PPQEGNKRSAR 188
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Search completed: September 25, 2005, 21:05:26
Job time : 120 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 25, 2005, 21:02:06 ; Search time 508 Seconds
(without alignments)
188.283 Million cell updates/sec

Title: US-09-874-140-2

Perfect score: 1206

Sequence: 1 MTQPASRRVVDPSNPPTFS.....KGQTLSTGSGNARSRRV 235

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Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	235	12	US-09-874-140-2
2	153.5	12.7	119	17	US-10-626-832-31
3	146	12.1	1367	15	US-10-320-797-3355
4	131	10.9	574	16	US-10-437-963-166255
5	130	10.8	1717	15	US-10-425-114-58581
6	128	10.6	1151	10	US-09-825-751A-79
7	128	10.6	1151	18	US-10-851-438-79
8	127.5	10.6	797	14	US-10-156-761-10907
9	127.5	10.6	907	9	US-09-328-599A-1
10	127	10.5	630	16	US-10-322-281-428
11	127	10.5	720	16	US-10-322-281-432

12	126.5	10.5	839	14	US-10-245-752-54	Sequence 54, Appl
13	126.5	10.5	839	14	US-10-245-859-54	Sequence 54, Appl
14	126.5	10.5	839	14	US-10-245-103-54	Sequence 54, Appl
15	126.5	10.5	839	14	US-10-245-107-54	Sequence 54, Appl
16	126.5	10.5	839	14	US-10-245-143-54	Sequence 54, Appl
17	126.5	10.5	839	14	US-10-245-771-54	Sequence 54, Appl
18	126.5	10.5	839	14	US-10-245-851-54	Sequence 54, Appl
19	126.5	10.5	839	14	US-10-245-883-54	Sequence 54, Appl
20	126.5	10.5	839	14	US-10-237-535-54	Sequence 54, Appl
21	126.5	10.5	839	14	US-10-238-183-54	Sequence 54, Appl
22	126.5	10.5	839	14	US-10-238-283-54	Sequence 54, Appl
23	126.5	10.5	839	14	US-10-238-370-54	Sequence 54, Appl
24	126.5	10.5	839	14	US-10-245-055-54	Sequence 54, Appl
25	126.5	10.5	839	14	US-10-245-147-54	Sequence 54, Appl
26	126.5	10.5	839	14	US-10-245-730-54	Sequence 54, Appl
27	126.5	10.5	839	14	US-10-245-739-54	Sequence 54, Appl
28	126.5	10.5	839	14	US-10-246-210-54	Sequence 54, Appl
29	126.5	10.5	839	14	US-10-239-196-54	Sequence 54, Appl
30	126.5	10.5	839	14	US-10-243-024-54	Sequence 54, Appl
31	126.5	10.5	839	14	US-10-243-409-54	Sequence 54, Appl
32	126.5	10.5	839	14	US-10-245-621-54	Sequence 54, Appl
33	126.5	10.5	839	14	US-10-245-880-54	Sequence 54, Appl
34	126.5	10.5	839	14	US-10-245-033-54	Sequence 54, Appl
35	126.5	10.5	839	14	US-10-243-095-54	Sequence 54, Appl
36	126.5	10.5	839	14	US-10-245-185-54	Sequence 54, Appl
37	126.5	10.5	839	14	US-10-245-427-54	Sequence 54, Appl
38	126.5	10.5	839	14	US-10-245-473-54	Sequence 54, Appl
39	126.5	10.5	839	14	US-10-245-770-54	Sequence 54, Appl
40	126.5	10.5	839	14	US-10-245-877-54	Sequence 54, Appl
41	126.5	10.5	839	14	US-10-246-976-54	Sequence 54, Appl
42	126.5	10.5	839	14	US-10-243-320-54	Sequence 54, Appl
43	126.5	10.5	839	14	US-10-242-743-54	Sequence 54, Appl
44	126.5	10.5	839	14	US-10-242-845-54	Sequence 54, Appl
45	126.5	10.5	839	14	US-10-237-636-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-09-874-140-2
; Sequence 2, Application US/09874140
; Publication No. US20050202413A1
; GENERAL INFORMATION:
; APPLICANT: EICKHORN, Markus
; APPLICANT: GICKLHORN, Dorothee
; APPLICANT: RADSAK, Klaus
; APPLICANT: HAUSER, Hans-Peter
; APPLICANT: GIESENDOERF, Bernhard
; TITLE OF INVENTION: VARICELLA ZOSTER VIRUS (VZV) IMMUNOREACTIVE PROTEIN
; FILE REFERENCE: 058315/0127
; CURRENT APPLICATION NUMBER: US/09/874,140
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/219,337
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: DE 197 57 765.2
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Varicella Zoster Virus
US-09-874-140-2

Query Match 100.0%; Score 1206; DB 12; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1e-80;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQPASRRVVDPSNPPTFSVEATAATPVALIRLLNASGPLQGHRRVADIARSIYTVG 60

Db 1 MTQPASRRVVDPSNPPTFSVEATAATPVALIRLLNASGPLQGHRRVADIARSIYTVG 60

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Db	61	AAASAARAPANANANTIRRTAMFAETDPMTWLRTVGLKRTFNPIIRPOPPNPSMSLGI	120
Qy	121	SGPTTLPQKTSADQSALQQPALAFSGSSPQHPPQTTTSASVQOQHVVVSGSSGGPOQ	180
Db	121	SGPTTLPQKTSADQSALQQPALAFSGSSPQHPPQTTTSASVQOQHVVVSGSSGGPOQ	180
Qy	181	GAGSSTVQPTTGSPPAAQGVPOSTPPPTQNTPOGKGQTLSTHTSGSNASRSRV	235
Db	181	GAGSSTVQPTTGSPPAAQGVPOSTPPPTQNTPOGKGQTLSTHTSGSNASRSRV	235

RESULT 2
US-10-626-832-31
Sequence 31, Application US/10626832
Publication No. US20050003342A1
GENERAL INFORMATION:
APPLICANT: Davis Poynter, Nick
APPLICANT: Nugent, Josephine
APPLICANT: Birch-Machin, Ian
APPLICANT: Allen, George P
TITLE OF INVENTION: Viral Marker
FILE REFERENCE: 620-262
CURRENT APPLICATION NUMBER: US/10/626,832
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 60/398,576
PRIOR FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 119
TYPE: PRT
ORGANISM: Equine herpesvirus 1
US-10-626-832-31

Query Match	12.7%	Score 153.5;	DB 17;	Length 119;
Best Local Similarity	31.1%;	Pred. No. 0.0086;		
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Qy	3	QPASSRVFDPNPTTFSVEATAATYPVALIRLLNASGFLQGPHRVDIADRSIIYT----	58	
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		: :: :	:	:
Db	6	QQQAQPAVENPADPPNIKAANFKMLPVDVITILN-----QNIDELDYTK-YTEDEI	56	
Qy	59	-----VGAAASARAPAHNVANTIRRTAMFAETDPMWLRTVGIKETFNPRIIRP	109	
Db	57	SEGLKOLFMTGARTWVSFQRHLKSLSVRDMFAQNDASTWARENIGIKATFFPRFMQP	115	

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RESULT 3
US-10-320-797-3355
; Sequence 3355, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3355
; LENGTH: 1367
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (357)..(357)

```

Db 473 MKSPS 477

RESULT 5

US-10-425-114-58581

Sequence 58581, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 58581

LENGTH: 717

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: UC-ZMFLB73099H11_FU1.pep

US-10-425-114-58581

Query Match 10.8%; Score 130; DB 15; Length 717;

Best Local Similarity 28.7%; Pred. No. 0.34; 57; Indels 52; Gaps 7;

Matches 50; Conservative 15; Mismatches 15

QY 93 RPTVGLKRTFNRIIRPQPNPMSLIGISGPTILPQKTSADQSALQOPALAFSGSSPQ 152

DB 489 QPFWGQGGY-----PQPDVPARPPYSGPQWPPRGAPADGSGYQAPAA-----S 534

QY 153 HPPPTTSASVQQQHVHVGSSG--QQ--PQQAQSSSTVQPTTGSPPAAQGVPO-----S 203

DB 535 YGPPSHPSAYGQTSYAATGSDGYAQGYPQGGQAPA--PYQSAAPAGYPQQQGGYA 592

QY 204 TPPTQNT-----PQGGKQGTLSHTGSGNAS 230

DB 593 QYPTQPAYGEAAQNASYGVQAPADPNYGSAYPQPGYPPGQATGQAGTAS 646

RESULT 6

US-09-825-751A-79

Sequence 79, Application US/09825751A

Publication No. US20030065140A1

GENERAL INFORMATION:

APPLICANT: CuraGen Corporation

APPLICANT: Vernet, Corine A.M.

APPLICANT: Fernandes, Elma R.

APPLICANT: Taupier, Raymond J.

APPLICANT: Quinn, Kerry E.

APPLICANT: Spytek, Kimberly A.

APPLICANT: Rastelli, Luca

APPLICANT: Herrman, John L.

TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 15966-750

CURRENT APPLICATION NUMBER: US/09/825,751A

CURRENT FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: 60/194,314

PRIOR FILING DATE: 2000-04-03

PRIOR APPLICATION NUMBER: 60/225,693

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 85

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 79

LENGTH: 1151

TYPE: PRT

ORGANISM: Gallus gallus

US-09-825-751A-79

Query Match 10.6%; Score 128; DB 18; Length 1151;

Best Local Similarity 28.2%; Pred. No. 0.8;

Matches 57; Conservative 22; Mismatches 81; Indels 42; Gaps 11;

QY 59 VGAA-----ASAAARAHNHNANTIRRTAMFAETDPTMTWLRPTVGLKRTFNRIIRP 109

DB 776 MGAATTPQSPMGAATQVTATSGNTMQVSPMGAAATPPQT---PSVGAAT-----P 825

QY 110 QPNPMSLIGISGPTILPQKTSADQSAL-QOPALAFSGSSPQHPP-----PQT---SA 161

DB 826 QPSPMGAATTLMSPMGAATTPQSPMGAVTTQPPMAATNTT-QPPMAASTPQSTPMGA 884

QY 162 SVGQQHVHVGSSGQQPQQAQSSSTVQPT-TGSP-----PAAQGVPO---STPPT 208

DB 885 ATTTQSPMGATTTQSPMGASTPQAPPTVAGSTPPPPPIPPSPTAQTSQPQMSKSPPPD 944

QY 209 QNTPQGGKQGTLSHTGSGNAS 230

DB 945 PPKAFSAAAT-SPAHHVANAS 965

RESULT 7

US-10-851-438-79

Sequence 79, Application US/10851438

Publication No. US20050153305A1

GENERAL INFORMATION:

APPLICANT: CuraGen Corporation

APPLICANT: Vernet, Corine A.M.

APPLICANT: Fernandes, Elma R.

APPLICANT: Taupier, Raymond J.

APPLICANT: Quinn, Kerry E.

APPLICANT: Spytek, Kimberly A.

APPLICANT: Rastelli, Luca

APPLICANT: Herrman, John L.

TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 15966-750

CURRENT APPLICATION NUMBER: US/10/851,438

CURRENT FILING DATE: 2004-05-21

PRIOR APPLICATION NUMBER: US/09/825,751

PRIOR FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: 60/194,314

PRIOR FILING DATE: 2000-04-03

PRIOR APPLICATION NUMBER: 60/225,693

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 85

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 79

LENGTH: 1151

TYPE: PRT

ORGANISM: Gallus gallus

US-10-851-438-79

Query Match 10.6%; Score 128; DB 18; Length 1151;

Best Local Similarity 28.2%; Pred. No. 0.8;

Matches 57; Conservative 22; Mismatches 81; Indels 42; Gaps 11;

QY 59 VGAA-----ASAAARAHNHNANTIRRTAMFAETDPTMTWLRPTVGLKRTFNRIIRP 109

DB 776 MGAATTPQSPMGAATQVTATSGNTMQVSPMGAAATPPQT---PSVGAAT-----P 825

QY 110 QPNPMSLIGISGPTILPQKTSADQSAL-QOPALAFSGSSPQHPP-----PQT---SA 161

DB 826 QPSPMGAATTLMSPMGAATTPQSPMGAVTTQPPMAATNTT-QPPMAASTPQSTPMGA 884

QY 162 SVGQQHVHVGSSGQQPQQAQSSSTVQPT-TGSP-----PAAQGVPO---STPPT 208

DB 885 ATTTQSPMGATTTQSPMGASTPQAPPTVAGSTPPPPPIPPSPTAQTSQPQMSKSPPPD 944

QY 209 QNTPQGGKQGTLSHTGSGNAS 230

DB 945 PPKAFSAAAT-SPAHHVANAS 965

Db 473 MKSPS 477

RESULT 5

US-10-425-114-58581

Sequence 58581, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 58581

LENGTH: 717

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: UC-ZMFLB73099H11_FU1.pep

US-10-425-114-58581

Query Match 10.8%; Score 130; DB 15; Length 717;

Best Local Similarity 28.7%; Pred. No. 0.34; 57; Indels 52; Gaps 7;

Matches 50; Conservative 15; Mismatches 15;

QY 93 RPTVGLKRTFNRIIRPQPNPMSLIGISGPTILPQKTSADQSALQQPAAAFSGSSPQ 152

DB 489 QPFWGQQGY-----PQPDVPARPPYSGPQWPPRGAPADGSGYQAPAA-----S 534

QY 153 HPPQRTTSASVQQQHVHVGSSG--QQ--PQQAQSSSTVQPTTGSPPAAQGVPO-----S 203

DB 535 YGPPSHPSAYGQTSYAATGSDGYAQGYPQGGQAPA--PYQSAAPAGYPQQQGGYA 592

QY 204 TPPTQNT-----PQGGKQTLSTGSGNAS 230

DB 593 QYPTQPAYGEAAQNASYGVQAPADPNYGSAYPQPGYPPGQATGQAGTAS 646

RESULT 6

US-09-825-751A-79

Sequence 79, Application US/09825751A

Publication No. US20030065140A1

GENERAL INFORMATION:

APPLICANT: CuraGen Corporation

APPLICANT: Vernet, Corine A.M.

APPLICANT: Fernandes, Elma R.

APPLICANT: Taupier, Raymond J.

APPLICANT: Quinn, Kerry E.

APPLICANT: Spytek, Kimberly A.

APPLICANT: Rastelli, Luca

APPLICANT: Herrman, John L.

TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 15966-750

CURRENT APPLICATION NUMBER: US/09/825,751A

CURRENT FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: 60/194,314

PRIOR FILING DATE: 2000-04-03

PRIOR APPLICATION NUMBER: 60/225,693

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 85

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 79

LENGTH: 1151

TYPE: PRT

ORGANISM: Gallus gallus

US-09-825-751A-79

Query Match 10.6%; Score 128; DB 18; Length 1151;

Best Local Similarity 28.2%; Pred. No. 0.8;

Matches 57; Conservative 22; Mismatches 81; Indels 42; Gaps 11;

QY 59 VGAA-----ASAAARAHNHNANTIRRTAMFAETDPTMTWLRTPTVGLKRTFNRIIRP 109

DB 776 MGAATTTQSPMGAATQVTATSGNTMQVSPMGAAATPPQT---PSVGAATT-----P 825

QY 110 QPNPMSLIGISGPTILPQKTSADQSAL-QQPAAAFSGSSPQHPP-----PQT---SA 161

DB 826 QPSPMGAATTLMSPMGAATTTQPSPMGAATTTQPPMAATNTT-QPPMAASTPQSTPMGA 884

QY 162 SVGQQHVHVGSSGQQPQQAQSSSTVQPT-TGSP-----PAAQGVPO---STPPT 208

DB 885 ATTTQSPMGAATTTQSPMGAATTTQPPMAATNTT-QPPMAASTPQSTPMGA 884

QY 209 QNTPQGGKQTLSTGSGNAS 230

DB 945 PPKAFSAAAT-SPAHHVANAS 965

RESULT 7

US-10-851-438-79

Sequence 79, Application US/10851438

Publication No. US20050153305A1

GENERAL INFORMATION:

APPLICANT: CuraGen Corporation

APPLICANT: Vernet, Corine A.M.

APPLICANT: Fernandes, Elma R.

APPLICANT: Taupier, Raymond J.

APPLICANT: Quinn, Kerry E.

APPLICANT: Spytek, Kimberly A.

APPLICANT: Rastelli, Luca

APPLICANT: Herrman, John L.

TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 15966-750

CURRENT APPLICATION NUMBER: US/10/851,438

CURRENT FILING DATE: 2004-05-21

PRIOR APPLICATION NUMBER: US/09/825,751

PRIOR FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: 60/194,314

PRIOR FILING DATE: 2000-04-03

PRIOR APPLICATION NUMBER: 60/225,693

PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 85

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 79

LENGTH: 1151

TYPE: PRT

ORGANISM: Gallus gallus

US-10-851-438-79

Query Match 10.6%; Score 128; DB 18; Length 1151;

Best Local Similarity 28.2%; Pred. No. 0.8;

Matches 57; Conservative 22; Mismatches 81; Indels 42; Gaps 11;

QY 59 VGAA-----ASAAARAHNHNANTIRRTAMFAETDPTMTWLRTPTVGLKRTFNRIIRP 109

DB 776 MGAATTTQSPMGAATQVTATSGNTMQVSPMGAAATPPQT---PSVGAATT-----P 825

QY 110 QPNPMSLIGISGPTILPQKTSADQSAL-QQPAAAFSGSSPQHPP-----PQT---SA 161

DB 826 QPSPMGAATTLMSPMGAATTTQPSPMGAATTTQPPMAATNTT-QPPMAASTPQSTPMGA 884

QY 162 SVGQQHVHVGSSGQQPQQAQSSSTVQPT-TGSP-----PAAQGVPO---STPPT 208

DB 885 ATTTQSPMGAATTTQSPMGAATTTQPPMAATNTT-QPPMAASTPQSTPMGA 884

QY 209 QNTPQGGKQTLSTGSGNAS 230

DB 945 PPKAFSAAAT-SPAHHVANAS 965

```
RESULT 8
US-10-156-761-10907
; Sequence 10907, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10907
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10907

Query Match      10.6%; Score 127.5; DB 14; Length 797;
Best Local Similarity 29.3%; Pred. No. 0.58;
Matches 61; Conservative 14; Mismatches 104; Indels 29; Gaps 8;

QY 36 LNASGPLQCHRVDIADARSIVTGAASAARARA--NENANTIRRTAMFAETDPMTWLR 93
Db 460 LRALRPLPFLPAAATPASPRAAARALPSPPTTAAATSPSMTLPPVWRR 519
QY 94 PTVGLKRTFNPRIIRPPNPMSLIGISGPTILPQKTSADQSALQOQPAALAFSGSSPOH 153
Db 520 PA-----RSSRP-PPRPS-----SRTASPTTRCSVWSSSPATRSVSASPTP 564
QY 154 PPTQTSASVGOQHVVSSGSGOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQ 212
Db 565 PPSRKPRST---RRPFSASSTTSRRTTSRTSSSTRRRPPTS---PASPPRPPSRTS 618
QY 213 QGKGQTLSTGOSGNASR-----SRRV 235
Db 619 SASSAAWTSRSTSSRRASRSTPRRV 646

RESULT 9
US-09-328-599A-1
; Sequence 1, Application US/09328599A
; Publication No. US20020119529A1
; GENERAL INFORMATION:
; APPLICANT: MOND, James J. and Lees, Andrew
; TITLE OF INVENTION: Enhancement of B Cell Activation by
; TITLE OF INVENTION: Co-ligation of Receptors for Antigen and Complement C3d
; TITLE OF INVENTION: Using EBV gp350/220 or EBV gp350/220 Peptide Adjuvants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/328,599A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B.
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 04995.6025-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 907 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-328-599A-1

Query Match      10.6%; Score 127.5; DB 9; Length 907;
Best Local Similarity 24.9%; Pred. No. 0.67;
Matches 64; Conservative 26; Mismatches 88; Indels 79; Gaps 14;

QY 2 TOPASSRVVFDP--SNPT---TFSVEAIAAYTPVALIRLLNASGLOPCHRVDIADARSI 56
Db 577 TSPTSAVTTTPNATSPTLGKTSPTSAVTTPP-----NATGP----- 614
QY 57 YTVGAASAARARAHNANTIRRTAMFAETDPMTWLRPTVGLKRTFNPRIIRPPNPMSM 116
Db 615 -TVGTSPOANA-TNH---TLGGTS-----PT-----PVTSPQPKNATS 648
QY 117 SLGISGPTILPQKTSADQSALQOQPAAL--AFSGSSPQHPP-----PQT TSA 161
Db 649 AVTTQHNITSSSTSSMSLRPSSNPETLSPSTDNSTSHMPLTSAHPGTGENITQVTPA 708
QY 162 SVGOQHVVSSGSGOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQ 218
Db 709 SI--STHVSTSS-PEPRGTTTSAAGSGNASTSTKPGEVNVTGKTPQNAATSPQAPSQ 765
QY 219 -----TLSHTGOSGNAS 230
Db 766 KTAVPTVTSTGKANST 782

RESULT 10
US-10-322-281-428
; Sequence 428, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 428
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-428

Query Match      10.5%; Score 127; DB 16; Length 630;
Best Local Similarity 28.0%; Pred. No. 0.48;
Matches 73; Conservative 18; Mismatches 96; Indels 74; Gaps 15;

QY 1 MTQPASSRVVFDPSNPTTFSVEAIAAYTPVALIRLLNASGLOP-----GHRVDIADAR 54
Db 200 MSQPT-----PAQPSFVGQPPPPPPVGVGAQAQSSAPLPPPPGAAATGPPMMAAQ 252
QY 55 SIYTVGAASAARARAHNANTIRRTAMFAETDPMTWLRPTVGLKRTFNPRIIRPPNP 113
```

Db 253 PSQPOGAGGGGQTLPPPTN-VTLAQPAMSLPPQP-----GPAVGAPAAQQOQFAYPQQOI 306
Qy 114 PMSLIGISGPTTLPOKTSADQSA-LQOPAALAFSGSSPQHP-PPQTTTAS-----V 163
Db 307 PPGHL-----LP--VQPSGQSEYLQOHVA-----GLQPPSPAQPSSTGAADATAATLPV 353
Qy 164 GQQQHWS-----GSSGQQ-----PQGAQSSTVQPTTGGSP-----PA 196
Db 354 GTGQWASSVGAQLMGASSQPSSEMAPRTGPAQGGQVAPCQPTGVPVATVGGVGVQVCLGPA 413
Qy 197 AQGVQPSSTPPPTQNTPOQGGK 217
Db 414 GAGQPSQSVPPP-----QMGSG 430

RESULT 11

US-10-322-281-432
; Sequence 432 Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 52945200100
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 432
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-432

Query Match 10.5%; Score 127; DB 16; Length 720;
Best Local Similarity 28.0%; Pred. No. 0.56; Mismatches 96; Indels 74; Gaps 15;
Matches 73; Conservative 18

Qy 1 MTQPASSRVFDPSPNTTFSVEAIAAYTPVALIRLLNAGGPIQP-----GHRVDIADAR 54
Db 200 MSQPT-----PAQPSFSGVQOQPPPPVGVGAQAQSSAPLPPPPGAATGQPQPMWAAQ 252
Qy 55 SIYTVGAASARARANNNANTIRTMFAETDPTWLRPTVGLKRTNP-RIRPQPPN 113
Db 253 PSQPOGAGGGGQTLPPPTN-VTLAQPAMSLPPQP-----GPAVGAPAAQQOQFAYPQQOI 306
Qy 114 PMSLIGISGPTTLPOKTSADQSA-LQOPAALAFSGSSPQHP-PPQTTTAS-----V 163
Db 307 PPGHL-----LP--VQPSGQSEYLQOHVA-----GLQPPSPAQPSSTGAADATAATLPV 353
Qy 164 GQQQHWS-----GSSGQQ-----PQGAQSSTVQPTTGGSP-----PA 196
Db 354 GTGQWASSVGAQLMGASSQPSSEMAPRTGPAQGGQVAPCQPTGVPVATVGGVGVQVCLGPA 413
Qy 197 AQGVQPSSTPPPTQNTPOQGGK 217
Db 414 GAGQPSQSVPPP-----QMGSG 430

RESULT 12

US-10-245-752-54
; Sequence 54 Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin

; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C66
; CURRENT APPLICATION NUMBER: US/10/245,752
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 54
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-245-752-54

Query Match 10.5%; Score 126.5; DB 14; Length 839;
Best Local Similarity 25.5%; Pred. No. 0.72;
Matches 76; Conservative 24; Mismatches 97; Indels 101; Gaps 16;

Qy 17 TTFSEVETAA-----YTPEVALIR-----LNASGPIQP-----GHRVDIADARS 55
Db 338 TQTVTEAANAAGSPRPFQSLYRGTVARGAGVGVKDAAPASQLRLTAQDPESDLNS 397
Qy 56 IYT-----VGAASAARA-----NHN-----ANTIRKTAMFAETDP 88
Db 398 AITVRIITHSHFRMEGEVLLTTTLAQAGAFVAEVAHNTVTSGTATTVIEIQVSEQBPP 457
Qy 89 MTWLRPTVGLKRTNPRIIRPQPPNSM-----SLGISGP-----TILPQKTS----- 132
Db 458 STEAGGTTGPWTSTTSEV--PRPPEPSQGPSTTSGGGTGPHPPSGTTLRPPTSTPGP 515
Qy 133 --AQOSALQQPAALAFSGSSPQHPPPQTT-----SASVGQQHVVSGSSQOQOQGAQ 183
Db 516 PGAENSTSHQPATP--GGDTAQTPKGTSPQMPPOVGTSTSHQPATPSGGAQTPEPGTS 573
Qy 184 -----SSTVQPTTGGSPAAQ-----GVFQSTPP-----PTQNTPOGGKQGT 219
Db 574 QPMPPSMGTSTSHQPATPGGTAQTPEAGTSQPMPPGNGTSTSHQPT--TPGGGTAQT 629

RESULT 13

US-10-245-859-54
; Sequence 54 Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria

```
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C78
; CURRENT APPLICATION NUMBER: US/10/245, 859
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 54
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-859-54

Query Match      10.5%; Score 126.5; DB 14; Length 839;
Best Local Similarity 25.5%; Pred. No. 0.72;
Matches 76; Conservative 24; Mismatches 97; Indels 101; Gaps 16;

QY 17 TTFSEVIAIA-----YTPVALIR-----LLNASGFLQP-----GHRVDIADARS 55
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QY 56 IYT-----VGAASAARARA-----NHN-----ANTIRRTAMFAETDP 88
Db 398 AITYRITNHSHFMEGEVLLTTTLAQAGAFYAEVAEHNVTSGTATTVIEIQVSEQEP 457
QY 89 MTWLRTVGLKRTFNRIIRPOPPNPSM-----SLGISGP-----TILPQKTQS----- 132
Db 458 STEAGTTGPTWTSTTSEV--PRPEFSQGPSTTSSGGGTGPHPPSGTTLRPTSTPGGP 515
QY 133 --ADQSALQQAALAFSGSSQHPPPQTT-----SASVGQOQHVVSGSSGQOQOQGAQ 183
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RESULT 14
US-10-245-103-54
; Sequence 54, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C112
; CURRENT APPLICATION NUMBER: US/10/245, 103
; CURRENT FILING DATE: 2002-09-17
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 54
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-54

Query Match      10.5%; Score 126.5; DB 14; Length 839;
Best Local Similarity 25.5%; Pred. No. 0.72;
Matches 76; Conservative 24; Mismatches 97; Indels 101; Gaps 16;

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Db 338 TQVTVENAAAGSPRPFSQSLYRGTVARGAGVGVVVKDAAAFSQPLRIQAQDPFSDLS 397
QY 56 IYT-----VGAASAARARA-----NHN-----ANTIRRTAMFAETDP 88
Db 398 AITYRITNHSHFMEGEVLLTTTLAQAGAFYAEVAEHNVTSGTATTVIEIQVSEQEP 457
QY 89 MTWLRTVGLKRTFNRIIRPOPPNPSM-----SLGISGP-----TILPQKTQS----- 132
Db 458 STEAGTTGPTWTSTTSEV--PRPEFSQGPSTTSSGGGTGPHPPSGTTLRPTSTPGGP 515
QY 133 --ADQSALQQAALAFSGSSQHPPPQTT-----SASVGQOQHVVSGSSGQOQOQGAQ 183
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QY 184 -----SSTVQPTTGPSPAAQ-----GVPQSTPP-----PTQNTPOGKGQOT 219
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; Sequence 54, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
```


APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C71
CURRENT APPLICATION NUMBER: US/10/245,107
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 54
LENGTH: 839
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-54

Query Match 10.5%; Score 126.5; DB 14; Length 839;
Best Local Similarity 25.5%; Pred. No. 0.72;
Matches 76; Conservative 24; Mismatches 97; Indels 101; Gaps 16;
Qy 17 TTFVSVEATAA-----YTPVALIR-----LLNASGPLOP-----GHRVDIADARS 55
Db 338 TQVTVEAAGSPRRFPQSLYRGTVARGAGVGVVVDAAAPSPQLRIQAOOPFSDLNS 397
Qy 56 IYT-----VGAASAARARA-----NIN-----ANTIRRTAMFAETDP 88
Db 398 AIYRITVHSHPRMEGEVLLTTTLAQACAFYAEVEAHNTVTSGTATTVIEIQVSEQEPP 457
Qy 89 MTWLRPTVGLKFTFNPIRPOPPNPSM-----SLGISGP-----TILPQKTS----- 132
Db 458 STEAGGTGCPWTSTTSEV--PRPPEPSQGPSTSSGGGTGHPHPSGTTLRPPTSSTPGGP 515
Qy 133 --ADOSALQQPALAFSGSSPHPPQTIT-----SASVGQOQHVVSGSSCQPPQGAQ 183
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Search completed: September 25, 2005, 21:42:37
Job time : 509 secs

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OM nucleic - nucleic search, using sw model

Run on: September 25, 2005, 21:05:32 ; Search time 3605 Seconds
(without alignments)
9475.985 Million cell updates/sec

Title: US-09-874-140-1
Perfect score: 705
Sequence: 1 atgacacacccgcgtc.....cttcagaagtcgtagggtg 705

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
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12: gb.sy.*
13: gb.un.*
14: gb.vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	705	100.0	705	6	AR161681 Sequence
3	705	100.0	705	6	E36500 Varicella-z
4	705	100.0	124883	14	AY548170 Human her
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6	705	100.0	124884	6	AR431491 Sequence
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14	181.2	25.7	124138	14	AF275348 Cercopith
15	40.4	5.7	151102	14	AF282130 Meleagrid
16	40.4	5.7	159160	14	AF291866 Meleagrid
17	40	5.7	125020	9	AF429315 Homo sapi
18	39.6	5.6	142533	2	AC138160 Rattus no
19	39.6	5.6	189442	10	AC119382 Rattus no

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	21	38.8	5.5	232869	10	AL603925	AL603925	Mouse DNA
	22	38.6	5.5	34971	9	HS367G8	Z97634	Human DNA s
C	23	38.6	5.5	133069	2	AC026836	AC026836	Homo sapi
	24	38.6	5.5	260418	9	AE006463	AE006463	Homo sapi
C	25	38.4	5.4	2000	6	AX655393	AX655393	Sequence
	26	38.4	5.4	2167	4	AY035849	AY035849	Sus scrofa
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	28	37.8	5.4	11166	2	AC014870	AC014870	Drosophila
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	31	37.8	5.4	159479	3	AC009735	AC009735	Drosophila
	32	37.8	5.4	299749	3	AE003606	AE003606	Drosophila
	33	37.4	5.3	124139	8	AC134930	AC134930	Oryza sativa
	34	37.2	5.3	3030	8	VCA429230	AJ429230	Volvox carterii
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	36	37.2	5.3	87076	9	AC005918	AC005918	Homo sapi
	37	37.2	5.3	178288	9	AC147017	AC147017	Pan trogl
C	38	37	5.2	302614	1	AE016778	AE016778	Pseudomonas
	39	36.8	5.2	300885	1	AE012559	AE012559	Xylella fastidiosa
C	40	36.6	5.2	922	8	AK071477	AK071477	Oryza sativa
	41	36.6	5.2	1882	8	AK106923	AK106923	Oryza sativa
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ALIGNMENTS

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LOCUS A94878
DEFINITION Sequence 2 from Patent EP0927759.
ACCESSION A94878
VERSION A94878.1 GI:6779075
KEYWORDS Human herpesvirus 3
ORGANISM Human herpesvirus 3
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
REFERENCE 1 (bases 1 to 705)
AUTHORS Giesendorf, B.D. and Bickmann, M.D.
TITLE Immunoreactive protein VP26 of Varicella Zoster Virus (VZV) and its diagnostic use
JOURNAL Patent: EP 0927759-A 2 07-JUL-1999;
DADE BEHRING MARBURG GMBH (DE)
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Best Local Similarity 100.0%; Pred. No. 6.2e-205;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGACACACCCGCGATCGTCGTGTAGTCCTTTGATCCAGCAACCCACCATTTTCG 60
Qy 61 GTGGAAGCAATTCGGCTTACACCCCGTTCCTTTATACGCTTTAAACCCAGTGGGA 120
Db 61 GTGGAAGCAATTCGGCTTACACCCCGTTCCTTTATACGCTTTAAACCCAGTGGGA 120
Qy 121 CCTTTGCAACCTGTGTACCCGCGTGTGGACATCGCTGATGCCAGAGCATTTACACCGTGGGA 180
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RESULT 2
LOCUS AR161681 705 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6258363.
ACCESSION AR161681
VERSION AR161681.1 GI:16228540
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 705)
AUTHORS Bickmann,M., Gicklhorn,D., Radeak,K., Hauser,H.-P. and Giesendorf,B.
TITLE Varicella zoster virus (VZV) immunoreactive protein VP26 and its diagnostic use
JOURNAL Patent: US 6258363-A 1 10-JUL-2001;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 6.2e-205;
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DB 121 CCTTTGCAACCTGGTCAACCGTGTGGACATCGCTGTGCGCAAGACGATTTACACCGTGGGA 180
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DB 661 TCACACACGGGCAATCTGGAAACGTTCAAGAGTCGTAGGGT 705

RESULT 3
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DEFINITION Varicella-zoster virus (VZV) immune reaction protein VP26 and diagnostic utilization thereof.
ACCESSION E36500
VERSION E36500.1 GI:13022697
KEYWORDS Human herpesvirus 3
SOURCE Human herpesvirus 3
ORGANISM Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
REFERENCE 1 (bases 1 to 705)
AUTHORS Markus,A., Dorotia,G., Klaus,R., Hanspater,H. and Bernhard,G.
TITLE Varicella-zoster virus (VZV) immune reaction protein VP26 and diagnostic utilization thereof
JOURNAL Patent: JP 1999243974-A 1 14-SEP-1999;
COMMENT DEIDO BERINGU MARUBURUKU GMBH
OS Varicella-zoster virus
PN JP 1999243974-A/1
PD 14-SEP-1999
PF 22-DEC-1998 JP 1998364934
PR 23-DEC-1997 DE 19757765.2
PI MARKUS AIKUWAN,DOROTIA GIKURUHORUN,KLAUS RATOZAKU, PI HANS-PATER HAUSER,
PI BERNHARD GIZENDORUFU
PC C12N15/09,C07K14/04,C07K16/08,C12Q1/68,G01N33/53,G01N33/569//
PC (C12N15/09,C12R1:92),C12N15/00,(C12N15/00,C12R1:92) CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..705
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FT Location/Qualifiers
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LOCUS	124883 bp	DNA	linear	VRL 14-JUN-2004
DEFINITION	Human herpesvirus 3 strain MSP, complete genome.			
ACCESSION	AY548170 AH009871 AY005330 AY005331 AY005332 AY005333 AY005334			
VERSION	AY005335 AY034034			
KEYWORDS	AY548170.1 GI:46981482			
SOURCE	Human herpesvirus 3			
ORGANISM	Human herpesvirus 3			
	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
	Alphaherpesvirinae; Varicellovirus.			
REFERENCE	1 (bases 1 to 124883)			
AUTHORS	Santos, R.A., Hatfield, C.C., Cole, N.L., Padilla, J.A., Moffat, J.F.,			

TITLE	Arvin, A.M., Ruyechan, W.T., Hay, J., and Grose, C. varicella-zoster virus gE escape mutant VZV-MSP exhibits an accelerated cell-to-cell spread phenotype in both infected cell cultures and SCID-hu mice
JOURNAL MEDLINE PUBMED	Virology 275 (2), 306-317 (2000)
REFERENCE	20455576
AUTHORS	10998331
TITLE	2. (bases 1 to 124883)
JOURNAL PUBMED	Grose, C., Tyler, S., Peters, G., Hiebert, J., Stephens, G.M., Ruyechan, W.T., Jackson, W., Storlie, J. and Tipples, G.A. Complete DNA Sequence Analyses of the First Two Varicella-Zoster Virus Glycoprotein E (D150N) Mutant Viruses Found in North America: Evolution of Genotypes with an Accelerated Cell Spread Phenotype
REFERENCE	J. Virol. 78 (13), 6799-6807 (2004)
AUTHORS	15194755
TITLE	3. (bases 1 to 124883)
JOURNAL PUBMED	Santos, R.A., Hatfield, C.C., Cole, N.L., Padilla, J.A., Moffat, J.F., Arvin, A.M., Ruyechan, W.T., Hay, J. and Grose, C. Direct Submission
REFERENCE	Submitted (10-JUN-2000) Department of Microbiology, University of Iowa, Iowa City, IA 52242, USA
AUTHORS	4. (bases 1 to 124883)
TITLE	Santos, R.A., Hatfield, C.C., Cole, N.L., Padilla, J.A., Moffat, J.F., Arvin, A.M., Ruyechan, W.T., Hay, J. and Grose, C. Direct Submission
JOURNAL PUBMED	Submitted (04-MAY-2001) Department of Microbiology, University of Iowa, Iowa City, IA 52242, USA
REFERENCE	Sequence update by submitter
AUTHORS	5. (bases 1 to 124883)
TITLE	Grose, C., Tyler, S., Peters, G., Hiebert, J., Stephens, G., Ruyechan, W., Jackson, W., Storlie, J. and Tipples, G.A. Direct Submission
JOURNAL PUBMED	Submitted (13-FEB-2004) Health Canada, National Microbiology Laboratory, 1015 Arlington Street, Winnipeg, Manitoba R3E 3P6, Canada
COMMENT	On or before May 4, 2004 this sequence version replaced GI:14030155, GI:10697346, GI:10697347, GI:13940791, GI:10697349, GI:10697350, GI:10697351, GI:14030846.
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Arvin, A.M., Ruyechan, W.T., Hay, J., and Grose, C.
Varicella-zoster virus GE escape mutant VZV-MSP exhibits an
accelerated cell-to-cell spread phenotype in both infected cell
cultures and SCID-hu mice
Virology 275 (2), 306-317 (2000)
20455576
10998331
2 (bases 1 to 124883)
Grose, C., Tyler, S., Peters, G., Hiebert, J., Stephens, G.M.,
Ruyechan, W.T., Jackson, W., Storlie, J., and Tipples, G.A.
Complete DNA Sequence Analyses of the First Two Varicella-Zoster
Virus Glycoprotein E (D150N) Mutant Viruses Found in North America:
Evolution of Genotypes with an Accelerated Cell Spread Phenotype
J. Virol. 78 (13), 6799-6807 (2004)
15194755
3 (bases 1 to 124883)
Santos, R.A., Hatfield, C.C., Cole, N.L., Padilla, J.A., Moffat, J.F.,
Arvin, A.M., Ruyechan, W.T., Hay, J., and Grose, C.
Direct Submission
Submitted (10-JUN-2000) Department of Microbiology, University of
Iowa, Iowa City, IA 52242, USA
4 (bases 1 to 124883)
Santos, R.A., Hatfield, C.C., Cole, N.L., Padilla, J.A., Moffat, J.F.,
Arvin, A.M., Ruyechan, W.T., Hay, J., and Grose, C.
Direct Submission
Submitted (04-MAY-2001) Department of Microbiology, University of
Iowa, Iowa City, IA 52242, USA
5 (bases 1 to 124883)
Grose, C., Tyler, S., Peters, G., Hiebert, J., Stephens, G.,
Ruyechan, W., Jackson, W., Storlie, J., and Tipples, G.A.
Direct Submission
Submitted (13-FEB-2004) Health Canada, National Microbiology
Laboratory, 1015 Arlington Street, Winnipeg, Manitoba R3E 3P6,
Canada
On or before May 4, 2004 this sequence version replaced
GI:14030155, GI:10697346, GI:10697347, GI:13940791, GI:10697349,
GI:10697350, GI:10697351, GI:14030846.
Location/Qualifiers
1. 124883
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/strain="MSP"
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Db 42733 CCCGCCGCTTGGCGTTTTCGGGATCATCCCGCAACACCCCGCCACCTCAAAACGACGTCG 42674
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RESULT 5
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LOCUS Sequence 76 from patent US 6528066.
DEFINITION AR283580
ACCESSION AR283580
VERSION AR283580.1 GI:29720465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 124884)
AUTHORS Grose,C.F. and Santos,R.
TITLE Variant varicella-zoster viruses and methods of use
JOURNAL Patent: US 6528066-A 76 04-MAR-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
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Qy 61 GTGGAAGCAATTGGCGCTTACACCCCGCTTCTTTAATACGACTTTTAAACGCCAGTGGG 120
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RESULT 6
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LOCUS Sequence 1 from patent US 6653069.
DEFINITION AR431491
ACCESSION AR431491
VERSION AR431491.1 GI:40193595
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 124884)
AUTHORS Gomi,Y., Sunamachi,H., Takahashi,M. and Yamanishi,K.
TITLE Method for quality control of an attenuated varicella live vaccine
JOURNAL Patent: US 6653069-A 1 25-NOV-2003;
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RESULT 9
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LOCUS Human herpesvirus 3 strain BC, complete genome.
DEFINITION
ACCESSION AY548171
VERSION AY548171.1 GI:46981409
KEYWORDS
SOURCE
ORGANISM
Human herpesvirus 3
Human herpesvirus 3
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
REFERENCE
1 (bases 1 to 125459)
Grose, C., Tyler, S., Peters, G., Hiebert, J., Stephens, G.M.,
Ruechman, W.T., Jackson, W., Storlie, J. and Tipples, G.A.
Complete DNA Sequence Analyses of the First Two Varicella-Zoster
Virus Glycoprotein E (D150N) Mutant Viruses Found in North America:
Evolution of Genotypes with an Accelerated Cell Spread Phenotype
J. Virol. 78 (13), 6799-6807 (2004)
PUBMED 15194755
2 (bases 1 to 125459)
Grose, C., Tyler, S., Peters, G., Hiebert, J., Stephens, G.,
Ruechman, W., Jackson, W., Storlie, J. and Tipples, G.A.
Direct Submission
Submitted (13-FEB-2004) Health Canada, National Microbiology
Laboratory, 1015 Arlington Street, Winnipeg, Manitoba R3E 3P6,
Canada
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Best Local Similarity 100.0%; Pred. No. 1.3e-204;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	43032	CCACAGTCTACCCCGCCCCCAACCCCAAAATACCCCGCGGGGTAAAGGACAGACTTG	42973
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RESULT 10	AB097932/c		
LOCUS	Human herpesvirus 3	125078 bp	DNA linear VRL 13-DEC-2002
DEFINITION	Human herpesvirus 3 ORF62 gene for IE62 transactivator, complete		
ACCESSION	AB097932		
VERSION	AB097932.1	GI:26665420	
KEYWORDS	Human herpesvirus 3		
SOURCE	Human herpesvirus 3		
ORGANISM	Alphaherpesvirinae; Varicelloviruses.		
REFERENCE	1	Gomi, Y., Sunamachi, H., Mori, Y., Nagaike, K., Takahashi, M. and Yamanishi, K.	
AUTHORS	Comparison of the complete DNA sequences of the Oka varicella vaccine and its parental virus		
TITLE	J. Virol. 76 (22), 11447-11459 (2002)		
JOURNAL	22276345		
MEDLINE	12388706		
PUBMED	2	(bases 1 to 125078)	
REFERENCE	Gomi, Y., Sunamachi, H., Nagaike, K., Mori, Y., Takahashi, M. and Yamanishi, K.		
AUTHORS	Direct Submission		
TITLE	Submitted (11-DEC-2002) Yasuyuki Gomi, Kanonji institute, the research foundation for microbial diseases of Osaka university, research division; 2-9-41 Yahata-cho, Kanonji-city, Kagawa 768-0062, Japan (E-mail: ygomim@mail.biken.or.jp, Tel: 81-875-25-4171 (ex. 620), Fax: 81-875-25-4843)		
JOURNAL	Location/Qualifiers		
FEATURES	1. .125078		
source			

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ORIGIN	Query Match	99.8%;	Score 703.4;	DB 14;	Length 125078;
	Best Local Similarity	99.9%;	Pred. No. 4.2e-204;		
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RESULT 11
AB097933/c
LOCUS
DEFINITION Human herpesvirus 3 ORF62 gene for 1862 transactivator, complete
ACCESSION AB097933
VERSION AB097933.1 GI:26665422
KEYWORDS
SOURCE Human herpesvirus 3
ORGANISM Human herpesvirus 3
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
1
Gomi, Y., Sunamachi, H., Mori, Y., Nagaike, K., Takahashi, M. and
Yamanishi, K.
Comparison of the complete DNA sequences of the Oka varicella
vaccine and its parental virus
J. Virol. 76 (22), 11447-11459 (2002)
22276345
12388706
2 (bases 1 to 125125)
Gomi, Y., Sunamachi, H., Nagaike, K., Mori, Y., Takahashi, M. and
Yamanishi, K.
Direct Submission
Submitted (11-DEC-2002) Yasuyuki Gomi, Kanonji institute, the
research foundation for microbial diseases of Osaka university,
research division; 2-9-41 Yahata-cho, Kanonji-city, Kagawa
768-0062, Japan (E-mail: ygomie@mail.biken.or.jp.
Tel: 81-875-25-4171 (ex.620), Fax: 81-875-25-4843)
Location/Qualifiers
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ORIGIN

Query Match 99.8%; Score 703.4; DB 14; Length 125125;
Best Local Similarity 99.9%; Pred. No. 4.2e-204;
Matches 704; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 12
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LOCUS
DEFINITION Sequence 2 from patent US 6653069.
ACCESSION AB431492
VERSION AR431492.1 GI:40193596

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 125157)
AUTHORS	Gomi,Y., Sunamachi,H., Takahashi,M. and Yamanishi,K.
TITLE	Method for quality control of an attenuated varicella live vaccine
JOURNAL	Patent: US 663069-A 2 25-NOV-2003;
FEATURES	Location/Qualifiers
source	1..125157
ORIGIN	/organism="unknown" /mol_type="genomic DNA"
Query Match	99.8%; Score 703.4; DB 6; Length 125157;
Best Local Similarity	99.9%; Pred. No. 4.2e-204;
Matches 704; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 ATGACACAACCCGCGATCGTCTCGTGTAGTCTTTTGATCCCGAGCAACCCACACATTTTCG 60
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LOCUS	
DEFINITION	Method for the quality control of attetunated varicella live vaccine.
ACCESSION	BD097171

VERSION	BD097171.1	GI:22642745
KEYWORDS	WO 0156600-A/2.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 125157)	
AUTHORS	Gomi,Y., Sunamachi,H., Takahashi,M. and Yamanishi,K.	
TITLE	Method for the quality control of attetunated varicella live vaccine	
JOURNAL	Patent: WO 0156600-A 2 09-AUG-2001;	
COMMENT	THE RESEARCH FOUNDATION FOR MICROBIAL DISEASES OF OSAKA UNIVERSITY, YASUYUKI GOMI,HIROKI SUNAMACHI,MICHIYAKI TAKAHASHI,KOICHI YAMANISHI OS Attenuated varicella virus Oka strain	
PN	WO 0156600-A/2	
PD	09-AUG-2001	
PF	31-JAN-2001	WO 2001JP000678
PR	31-JAN-2000	JP OOP 62734
PI	YASUYUKI GOMI,HIROKI SUNAMACHI,MICHIYAKI TAKAHASHI,KOICHI YAMANISHI	
PC	A61K39/25,A61P31/22,C12N15/38,C12N7/00,G01N33/15	CC Method
for the quality control of attetunated varicella live CC		
vacine		
FH	Key	Location/Qualifiers
FT	source	1..125157
FEATURES	Location/Qualifiers	
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Matches 704; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
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LOCUS		
DEFINITION	Method for the quality control of attetunated varicella live vaccine.	
ACCESSION	BD097171	

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RESULT 14
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LOCUS Cercopithecine herpesvirus 7, complete genome.
DEFINITION AF275348
ACCESSION AF275348
VERSION AF275348.2 GI:13186283
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gray, W.L., Starnes, B., White, M.W., and Mahalingam, R.
TITLE The DNA sequence of the simian varicella virus genome
JOURNAL Virology 284 (1), 123-130 (2001)
MEDLINE 21251382
PUBMED 11352673
REFERENCE
AUTHORS Gray, W.L., Starnes, H.B., White, M.W., Ashburn, C.V. and Mahalingam, R.
TITLE Complete Sequence of the Simian Varicella Virus Genome
JOURNAL Unpublished
REFERENCE
AUTHORS Gray, W.L., Starnes, H.B., White, M.W., Ashburn, C.V. and Mahalingam, R.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-2000) Microbiology/Immunology, University of Arkansas for Medical Sciences, 4301 W. Markham St., Little Rock, AR 72205, USA
REFERENCE
AUTHORS Gray, W.L., Starnes, H.B., White, M.W., Ashburn, C.V. and Mahalingam, R.
TITLE Direct Submission
JOURNAL Submitted (02-MAR-2001) Microbiology/Immunology, University of Arkansas for Medical Sciences, 4301 W. Markham St., Little Rock, AR 72205, USA
REMARK
COMMENT Sequence update by submitter
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Query Match		5.7%;	Score 40.4;	DB 14;	Length 151102;
Best Local Similarity		61.3%;	Pred. No. 1.8;		
Matches 65;		Conservative 0;	Mismatches 41;	Indels 0;	Gaps 0;
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QY	272	GGTTAAGACCAACGGTTGGCTTAAACGTCACGTTTAAACCCGGGTAT	317		
Db	63626	GGATCAGACCATCCATTGGATTAAAGCGCACCTACCCACCGGGTAT	63671		

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Job time : 3613 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-874-140-1

Perfect score: 705

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004as.*
13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	705	100.0	705	2	Aax78759 VZV VP26
2	705	100.0	124884	5	Aah74201 Nucleotid
3	705	100.0	124884	10	Adal4878 Human her
4	705	100.0	124884	11	Adl99489 Varicella
5	703.4	99.8	125157	5	Aah74202 Nucleotid
6	38.4	5.4	2000	8	Ada71938 Rice gene
7	37.8	5.4	144411	12	Adp74214 Equine he
8	37.8	5.4	144486	12	Adp74215 Equine he
9	37.8	5.4	145444	12	Adp74213 Equine he
10	37.8	5.4	145596	12	Adp74202 Equine he
11	37.6	5.3	4590	5	Aah24065 Yeast AOD
12	37	5.2	711	8	Aca43990 Prokaryot
13	36.2	5.1	110000	4	Continuation (28 o
14	36.2	5.1	110000	4	Continuation (29 o
15	36.2	5.1	110000	4	Continuation (28 o
16	36.2	5.1	110000	4	Continuation (29 o
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20	35.8	5.1	110000	4	Continuation (20 o

21	35.6	5.0	1222	10	ADD29744	Add29744 Mouse tum
22	35.6	5.0	13416	10	AAAD55815	Aad55815 Micromono
23	35.6	5.0	28874	3	AAA81505	Aaa81505 N. mening
24	35.6	5.0	60196	10	AAAD55810	Aad55810 Micromono
25	35.6	5.0	110000	3	AAA81490_07	Continuation (8 of
26	35.6	5.0	110000	3	AAA81490_08	Continuation (9 of
27	35.6	5.0	110000	4	AAI96882_22	Continuation (23 o
28	35.6	5.0	110000	4	AAI96883_22	Continuation (23 o
29	35.6	5.0	349980	3	AAF21608	Aaf21608 Neisseria
30	35.4	5.0	646	6	ABQ46950	Abq46950 Oligonuc1
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32	35.2	5.0	557	6	ABQ43461	Abq43461 Oligonuc1
33	35.2	5.0	557	6	ABQ43460	Abq43460 Oligonuc1
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35	34.6	4.9	11238	10	AAAD55817	Aad55817 Micromono
36	34.6	4.9	12531	4	AAAS9530	Aas9530 Propionib
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38	34.4	4.9	464	8	ABQ84714	Abq84714 Ostrinia
39	34.4	4.9	110000	4	AAI96883_39	Continuation (40 o
40	34.2	4.9	597	4	AAF22575	Aaf22575 Human bre
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42	34.2	4.9	54732	13	ABD33335	Abd33335 Human can
43	34	4.8	604	6	ABQ29893	Abq29893 Oligonuc1
44	34	4.8	604	6	ABQ29892	Abq29892 Oligonuc1
45	34	4.8	642	2	AAV23478	Aav23478 Pseudomon

ALIGNMENTS

RESULT 1

AAAX78759	
ID	AAAX78759 standard; DNA; 705 BP.
AC	AAAX78759;
XX	
DT	03-SEP-1999 (first entry)
XX	
DE	VZV VP26 DNA.
XX	
KW	VP26; immunoreactive protein; immunoassay; detection; anti-VZV; antibody;
KW	ds.
XX	
OS	Human herpesvirus 3.
XX	
PN	DE19757765-AL.
XX	
PD	24-JUN-1999.
XX	
PF	23-DEC-1997; 97DE-01057765.
XX	
PR	23-DEC-1997; 97DE-01057765.
XX	
PA	(DADE-) DADE BEHRING MARBURG GMBH.
XX	
PI	Eickmann M, Gicklhorn D, Radsak K, Hauser H, Giesendorf B;
XX	
DR	WPI; 1999-358931/31.
DR	P-PSDB; AAY25337.
XX	
PT	Varicella zoster virus VP26 peptide - and corresponding nucleic acid,
PT	useful for diagnosis of VZV infections.
XX	
PS	Claim 5; Page 5-7; 12pp; German.
XX	
CC	This invention describes a novel immunoreactive peptide comprising amino
CC	acids 12-235 of varicella zoster virus (VZV) protein VP26, and a nucleic
CC	acid encoding the peptide. Also claimed is a nucleic acid corresponding
CC	to a defined DNA sequence of 705 bp given in the specification, coding
CC	for amino acids 1-235 of VZV VP26. The peptide can be used in
CC	immunoassays for detecting anti-VZV antibodies. The nucleic acid can be
CC	used in hybridisation assays for detecting VZV
XX	


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Db 42538 CCACAGTCTACCCCGCCGCCCCAACCCAAATAATACCCCGAGGGGGGTAAAGGACAGACCTTG 42479
Qy 661 TCACACAGGGGACAAATCTGGAAACGCTTCAAGAAAGTCGTAGGGTG 705
Db 42478 TCACACAGGGGACAAATCTGGAAACGCTTCAAGAAAGTCGTAGGGTG 42434

RESULT 3
ADAL4878/c
ID ADAL4878 standard; DNA; 124884 BP.
XX
AC ADAL4878;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human herpesvirus 3 DNA.
XX
KW ds; varicella zoster virus; VZV; human herpesvirus 3; vaccine;
KW chicken pox; shingles.
XX
OS Human herpesvirus 3.
XX
PN US6528066-B1.
XX
PD 04-MAR-2003.
XX
PF 14-SEP-2000; 2000US-00661596.
XX
PR 14-SEP-1999; 99US-0153779P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Grose CF, Santos R;
XX
WPI; 2003-361635/34.
XX
New isolated polynucleotide isolated from varicella zoster virus, useful
PT for diagnosing a disease, for instance chicken pox and shingles, caused
PT by the virus.
XX
PS Disclosure; Col 61-168; 98pp; English.
XX
The invention relates to an isolated polynucleotide isolated from human
CC herpesvirus 3 (varicella zoster virus (VZV)). The polynucleotide is
CC useful for creating kits for detecting antibodies that specifically bind
CC to VZV polypeptide, for detecting the presence of VZV in an animal, for a
CC vaccine composition that includes a modified attenuated VZV, for
CC producing a modified attenuated VZV, for detecting VZV, such as VZV-MSP,
CC having a single nucleotide polymorphism in open reading frame (ORF) 68,
CC or for diagnosing a disease, for instance chicken pox and shingles,
CC caused by VZV. The present sequence represents human herpesvirus 3 DNA.
XX
SQ Sequence 124884 BP; 33789 A; 29295 C; 28177 G; 33623 T; 0 U; 0 Other;

Query Match 100.0%; Score 705; DB 10; Length 124884;
Best Local Similarity 100.0%; Pred. No. 3.3e-210;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGACACAAACCGGATCGTCTGCTAGTCTTTGATCCGACCAACCCACACATTTTCG 60
Db 43138 ATGACACAAACCGGATCGTCTGCTAGTCTTTGATCCGACCAACCCACACATTTTCG 43079

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Db 43078 GTGGAAGCAATTTGGGCTTACACCCCGCTTGTCTTAATACGACTTTTAAACGCCAGTGGGA 43019

Qy 121 CCTTTGCAACTGGTCAACCGTGTGACATCGCTGATGCCAGAAGCATTTACACCGTGGGA 180
Db 43018 CCTTTGCAACTGGTCAACCGTGTGACATCGCTGATGCCAGAAGCATTTACACCGTGGGA 42959

Qy 181 GCCGGGCGAGTGGCGCGGTGCAGCGCTAACCAATGCAATACGATACGCGGAACG 240
Db 42958 GCCGGGCGAGTGGCGCGGTGCAGCGCTAACCAATGCAATACGATACGCGGAACG 42899
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Qy 301 ACGTTTAAACCGGCGTATTATACGACCAACACCCCAATCCATCATGAGTTTGGGAATC 360
Db 42838 ACGTTTAAACCGGCGTATTATACGACCAACACCCCAATCCATCATGAGTTTGGGAATC 42779
Qy 361 TCGGGGCTACTATATTATTCGCGCAAAAACACAGAGCGCCGATCAGTCTGCTTTTCAACAG 420
Db 42778 TCGGGGCTACTATATTATTCGCGCAAAAACACAGAGCGCCGATCAGTCTGCTTTTCAACAG 42719
Qy 421 CCGCGCGGTTGGCGTTTTCGGGATCATCCCGGCAACACCCCCACCTCAACAGACGTCG 480
Db 42718 CCGCGCGGTTGGCGTTTTCGGGATCATCCCGGCAACACCCCCACCTCAACAGACGTCG 42659
Qy 481 GCATCCGTTGGACAAACAGCAACAGCTGTCGCGGTCCTTCTGACAAACACCCCAACAG 540
Db 42658 GCATCCGTTGGACAAACAGCAACAGCTGTCGCGGTCCTTCTGACAAACACCCCAACAG 42599
Qy 541 GGAGCAGTCAAGCACTGTCCAGCCCAACACCGGATCACCGCCCGCGCCCAAGCGGTG 600
Db 42598 GGAGCAGTCAAGCACTGTCCAGCCCAACACCGGATCACCGCCCGCGCCCAAGCGGTG 42539
Qy 601 CCACAGTCTACCCGCGCCCAACCCCAAAATACCCCGGAGGGGTAAAGGACAGACCTTG 660
Db 42538 CCACAGTCTACCCGCGCCCAACCCCAAAATACCCCGGAGGGGTAAAGGACAGACCTTG 42479
Qy 661 TCACACAGGGGACAACTCTGGAAACGCTTCAAGAGTCTAGGGTG 705
Db 42478 TCACACAGGGGACAACTCTGGAAACGCTTCAAGAGTCTAGGGTG 42434

RESULT 4
ADL99489/c
ID ADL99489 standard; DNA; 124884 BP.
XX
AC ADL99489;
XX
DT 20-MAY-2004 (first entry)
XX
Varicella-Zoster virus complete genome.
XX
Varicella-Zoster virus; ds; ORF68; ORF37; vaccine; VZV infection; SNP;
KW single nucleotide polymorphism.
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OS Human herpesvirus 3.
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FT /*standard_name= "Single nucleotide polymorphism"
FT variation /*tag= f
FT /*standard_name= "Single nucleotide polymorphism"
FT variation /*tag= g
FT /*standard_name= "Single nucleotide polymorphism"
FT /note= "Claimed in claim 62"
```

US2003166168-A1.
04-SEP-2003.
06-NOV-2002; 2002US-00288823.
14-SEP-1999; 99US-0153779P.
14-SEP-2000; 2000US-00661596.
(IOWA) UNIV IOWA RES FOUND.
Grose CF, Santos R;
WPI: 2003-898077/82.
GENBANK; X04370.

Detecting antibodies that bind to a varicella zoster polypeptide with polymorphisms in ORF37 or ORF68 comprises contacting sample with viral preparation having polymorphism and detecting presence of complex.

Claim 17; Page; 33pp; English.

The invention relates to detecting antibodies that specifically bind to a varicella zoster polypeptide, comprising contacting a sample having an antibody with a preparation comprising a varicella zoster polypeptide having a polymorphism to form a mixture and detecting the presence or absence of the complex. The polypeptide is encoded by a polymorphism of open reading frame 37 (ORF37) and/or ORF68. Also included are a kit for detecting antibodies that specifically bind to a varicella zoster polypeptide, a method for detecting the presence of a varicella zoster virus in an animal, a method for diagnosing a disease caused by varicella zoster virus, a method for detecting a varicella zoster virus having a single nucleotide polymorphism (SNP) in ORF68, a vaccine composition comprising a modified attenuated varicella zoster virus having the ATCC designation VR-795 where the nucleotide sequence of the virus has been modified to contain an SNP, a method for producing a modified attenuated varicella zoster virus having the ATCC designation VR-795, an isolated polynucleotide having the nucleotide sequence of nucleotide 66074 to 68599 of GenBank X04370 (with the proviso that nucleotide 66879 is a thymine) or nucleotides 115808 to 117679 of GenBank Accession X04370 (with the proviso that nucleotide 116255 is an adenine), an isolated polypeptide encoded by the polynucleotide and a virus having the designation VZV-MSP, VZV-VSD, VZV-VIA and/or VZV-Iceland. The methods and compositions of the present invention are useful for diagnosing, detecting and/or treating varicella zoster virus (VZV) infection. The present sequence is the VZV complete genome.

Query Match 100.0%; Score 705; DB 11; Length 124884;
Best Local Similarity 100.0%; Pred. No. 3.3e-210;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGACACACCGCATCGTCTCGTGTAGTCTTTGATCCCGACCAACCCACCAATTTTCG 60
43138 ATGACACACCGCATCGTCTCGTGTAGTCTTTGATCCCGACCAACCCACCAATTTTCG 43079

61 GTGGAAGCAATTGCGGCTTACACCCCGTGTCTTTAATACGACTTTTAAACGCGAGTGA 120
43078 GTGGAAGCAATTGCGGCTTACACCCCGTGTCTTTAATACGACTTTTAAACGCGAGTGA 43019

121 CTTTTCACACCTGTCACCGTGTGGACATCGTGTATGCCAGAGCAATTTACACCGTGGGA 180
43018 CTTTTCACACCTGTCACCGTGTGGACATCGTGTATGCCAGAGCAATTTACACCGTGGGA 42959

181 GCGCGCGCCAGTGC CGCGGTGCACGCGCTAACCAATAATGCAATACGATACGCGGAACG 240
42958 GCGCGCGCCAGTGC CGCGGTGCACGCGCTAACCAATAATGCAATACGATACGCGGAACG 42899

241 GCCATGTTTGGCGAGACTGACCTATGACATGGTTAAGACCAACGTTGGCTTAAACGT 300
42898 GCCATGTTTGGCGAGACTGACCTATGACATGGTTAAGACCAACGTTGGCTTAAACGT 42839

QY 301 ACGTTTAAACCGCGTATTATATACGACCAACAACCCCAAAATCCATCCATGAGTTTGGAAATC 360
DB 42838 ACGTTTAAACCGCGTATTATATACGACCAACAACCCCAAAATCCATCCATGAGTTTGGAAATC 42779

QY 361 TCGGGGCTTACTATATTCGCCGCAAAAAACACAGAGCGCGGATCAGTCTGCTTTTCAACAG 420
DB 42778 TCGGGGCTTACTATATTCGCCGCAAAAAACACAGAGCGCGGATCAGTCTGCTTTTCAACAG 42719

QY 421 CCCGCCGCTTGGCGTGTTCGGGATCATCCCGGCAACACCCCACTTCAACGAGCTCG 480
DB 42718 CCCGCCGCTTGGCGTGTTCGGGATCATCCCGGCAACACCCCACTTCAACGAGCTCG 42659

QY 481 GCATCCGTTGGACAACAGCAACACGCTGTGTGCGGGTCTTCTGGACAACAACCGCAACAG 540
DB 42658 GCATCCGTTGGACAACAGCAACACGCTGTGTGCGGGTCTTCTGGACAACAACCGCAACAG 42599

QY 541 GGAGCACAGTCAAGCACTGTCCAGCAACAACCGGATCACCGCCCGCGCCCAAGCGGTG 600
DB 42598 GGAGCACAGTCAAGCACTGTCCAGCAACAACCGGATCACCGCCCGCGCCCAAGCGGTG 42539

QY 601 CCACAGTCTACCCCGCCGCCCAACCAAAATACCCCGAGGGGGTAAAGGACAGACCTTG 660
DB 42538 CCACAGTCTACCCCGCCGCCCAACCAAAATACCCCGAGGGGGTAAAGGACAGACCTTG 42479

QY 661 TCACACACGGGACAATCTGGAAAACGCTTCAAGAACTCGTAGGGTG 705
DB 42478 TCACACACGGGACAATCTGGAAAACGCTTCAAGAACTCGTAGGGTG 42434

RESULT 5
AAH74202/c
ID AAH74202 standard; DNA; 125157 BP.
XX AAH74202;
AC AAH74202;
DT 15-OCT-2001 (first entry)
XX Nucleotide sequence of the Varicella virus Oka strain.
KW Oka strain; pox vaccine; vaccine; poxvirus disease; chickenpox; ss.
OS Varicella virus.
XX WO200156600-A1.
XX 09-AUG-2001.
XX 31-JAN-2001; 2001WO-JP000678.
XX 31-JAN-2000; 2000JP-00062734.
XX (OSAU) UNIV OSAKA.
XX Gomi Y, Sunamachi H, Takahashi M, Yamanishi K;
WPI: 2001-488845/53.
XX Method for checking absence of mutation at specific positions of varicella virus genome for quality control of attenuated live varicella vaccine.
XX Disclosure; Page 106-150; 158pp; Japanese.
XX The present sequence represents the nucleotide sequence of Varicella virus, Oka strain. The specification describes a method for the quality control of an attenuated pox vaccine, characterised in that the DNA sequence of specific parts of the viral genome in a sample is determined and proved to be conserved rather than mutated in comparison with the same parts of a reference viral genome. The method is useful for quality control of vaccines for use in the prevention of poxvirus diseases such as chickenpox
XX

SQ Sequence 125157 BP; 33776 A; 29439 C; 28285 G; 33624 T; 0 U; 33 Other;
Query Match 99.8%; Score 703.4; DB 5; Length 125157;
Best Local Similarity 99.9%; Pred. No. 1e-209;
Matches 704; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGACACACCGCGATCGTCTGCTGTAGTCTTTGATCCAGCAACCCACACATTTTCG 60
DB 43113 ATGACACACCGCGATCGTCTGCTGTAGTCTTTGATCCAGCAACCCACACATTTTCG 43054
QY 61 GTGGAAGCAATTTGGCGCTTACACCCCGTGTCTTTAATACGACTTTTAAACGCCAGTGA 120
DB 43053 GTGGAAGCAATTTGGCGCTTACACCCCGTGTCTTTAATACGACTTTTAAACGCCAGTGA 42994
QY 121 CCTTTGCAACCTGCTCACCCTGTGACATCGCTGATGCCAGAAGCATTTACACCGTGGGA 180
DB 42993 CCTTTGCAACCTGCTCACCCTGTGACATCGCTGATGCCAGAAGCATTTACACCGTGGGA 42934
QY 181 GCCCGCGCAGTGC CGCGCGGTGACGCGCTAACCTAATGCAATACGATACGCCGAACG 240
DB 42933 GCCCGCGCAGTGC CGCGCGGTGACGCGCTAACCTAATGCAATACGATACGCCGAACG 42874
QY 241 GCCATGTTTGGCGAGACTGACCTATGACATGCTTAAAGCAACCGTTGGCTTAAACGCT 300
DB 42873 GCCATGTTTGGCGAGACTGACCTATGACATGCTTAAAGCAACCGTTGGCTTAAACGCT 42814
QY 301 ACGTTTAAACCGCGTATTATAGACACCAACCCCAATCCATCATGATTTGGGAATC 360
DB 42813 ACGTTTAAACCGCGTATTATAGACACCAACCCCAATCCATCATGATTTGGGAATC 42754
QY 361 TCGGGGCTTACTATATTCGCGCAAAAAACACAGAGCGCGATCAGTCTGCTTTTACACAG 420
DB 42753 TCGGGGCTTACTATATTCGCGCAAAAAACACAGAGCGCGATCAGTCTGCTTTTACACAG 42694
QY 421 CCGCGCGGTGGCGTTTTCGGGATCATCCCGCAACACCCCCACCTCAACACGCTCG 480
DB 42693 CCGCGCGGTGGCGTTTTCGGGATCATCCCGCAACACCCCCACCTCAACACGCTCG 42634
QY 481 GCATCCGTTGGACAAACAGCAACAGTGTGTGCGGGTCTTCTGGAACAACACCGCAACAG 540
DB 42633 GCATCCGTTGGACAAACAGCAACAGTGTGTGCGGGTCTTCTGGAACAACACCGCAACAG 42574
QY 541 GGAGCAGTCAAGCACTGTCTCAGCCAAACACCGGATCACCGCCCGCGCCCAAGGCGTG 600
DB 42573 GGAGCAGTCAAGCACTGTCTCAGCCAAACACCGGATCACCGCCCGCGCCCAAGGCGTG 42514
QY 601 CCACAGTCTACCCCGCCCAACCCCAATATACCCCGAGGGGGTAAAGGACAGACCTTG 660
DB 42513 CCACAGTCTACCCCGCCCAACCCCAATATACCCCGAGGGGGTAAAGGACAGACCTTG 42454
QY 661 TCACACAGGGACATCTGGAACCGCTTCAAGAGTCTGAGGGTG 705
DB 42453 TCACACAGGGACATCTGGAACCGCTTCAAGAGTCTGAGGGTG 42409

RESULT 6

ADA71938/c
ID ADA71938 standard; DNA; 2000 BP.
XX ADA71938;
AC ADA71938;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 5263.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; da.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.
XX 22-JUN-2001; 2001WO-IB001105.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
XX
XX Identifying at least one gene involved in plant resistance or response to
XX pathogenic infection for conferring resistance or tolerance to a plant to
XX bacterial, fungal or viral infection by determining or detecting plant
XX gene expression.
XX
XX Claim 27; SEQ ID NO 5263; 899pp; English.
XX
XX The present invention relates to a method (M1) for identifying genes
XX involved in plant resistance or response to pathogenic infection. M1
XX comprises identifying a gene whose expression is significantly altered in
XX the incompatible interaction of plant gene expression relative to
XX expression of the gene in an uninfected plant, in a mutant plant that
XX does not express a gene associated with response to pathogenic infection,
XX or in a corresponding incompatible or compatible interaction. (M1) is
XX useful for conferring resistance to resistance or tolerance to a plant to
XX bacterial, fungal or viral infection. The present sequence was used to
XX illustrate the invention.
XX
XX Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
XX
XX Query Match 5.4%; Score 38.4; DB 8; Length 2000;
XX Best Local Similarity 10.8%; Pred. No. 0.41;
XX Matches 63; Conservative 268; Mismatches 249; Indels 6; Gaps 3;
QY 118 GGACCTTTGCAACCTGCTACCGTGTGGACATCGCTGATGCAGAGCATTTACACCGTG 177
DB 602 GKMTCTMYTSMKSTRSRKMRWMSRMVYMKRKRKRYMYMKWKTWRRCMCRYW 543
QY 178 GGAGCCCGCGCAGTCCGCGCGTGCACCGCTAACCATATGCAAAATACGATACCGCA 237
DB 542 GYTWYTSRSMYTGKRYKARYTSRRYMYWYKRYKRYMYWYKRYMYWYKRYMYWYKRY 484
QY 238 ACGCCGCTATGTTGCGAGACTGACCTATGATGCTTAAACCAACCGTGTGCTTAA 297
DB 483 CKKCCYAMCWAAAGSMWYKYSKMRMSTKYMWSMYKCRSMYKAGCYGCRMW 424
QY 298 CGTACGTTTAAACCGCGTATTATACGACAC - AACCCCAAAATCCATCCTGATTTGG 355
DB 423 TYSYGYMKWYTMGSYKYSRYMYWYKRYMYWYKRYMYWYKRYMYWYKRYMYWYKRY 364
QY 356 GAATCTCGGGCCTACTATATGCGGCAAAAAACACAGAGCGCGATCAGTCTGCTTAC 415
DB 363 YKRGTMWSYKYSYKRYKRYKRYKRYKRYKRYKRYKRYKRYKRYKRYKRYKRYKRY 304
QY 416 AACAGCCGCGCGTGTGCGGCTTTCGGGATCATCCCGCAACACCCCGCTCAACGGA 475
DB 303 YRKGWYSRRSMET - - - AGKWRWSRWSRWSRWSRWSRWSRWSRWSRWSRWSR 247
QY 476 CGTCGGCATCCGTTGGACAAACACAGCGTGTGCGGGTCTTCTGGAACAACACCGC 535
DB 246 WSRSAKRTYKYSTSRRAKMRACRMYSAKRYSRYSYCGSCYSGSKWYKSKSCM 187
QY 536 AACAGGAGGACAGTCAAGCATCTCCAGCAACACCGGATCAGCGCGCGCGCGCAAG 595
DB 186 RMTCSWCSCTCYGAMCSCCMWMSGCGYTRGWKWRKRYKRYKRYKRYKRYKRYKRY 127
QY 596 GCGTGCCACAGTCTACCCCGCCCAACCAAAATACCCCGAGGGGGTAAAGGACAGA 655
DB 126 CSYTGYYRYCKYKYSYKRYKRYKRYKRYKRYKRYKRYKRYKRYKRYKRYKRYKRY 67
QY 656 CCTTGTACACACGCGGACAAATCTGGAAACCGCTTCAAGAAAGTCGTAG 701

KW	virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;
KW	EHV-associated condition; Equine herpesvirus 4; EHV4; ds; mutant; mutein.
XX	
OS	Equine herpesvirus 4.
OS	Synthetic.
XX	
PX	US2004109873-A1.
XX	
PD	10-JUN-2004.
XX	
PF	21-JUL-2003; 2003US-00624149.
XX	
PR	19-JUL-2002; 2002DE-01033064.
PR	14-AUG-2002; 2002US-0403282P.
PR	11-APR-2003; 2003DE-01017008.
XX	(BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
PA	New recombinant equine herpes (EHV) virus free of heterologous elements,
PI	and where protein GM has been deleted, useful as a vaccine for treating
PI	or preventing EHV infections.
XX	
PI	Neubauer A, Ziegler C;
DR	WPI; 2004-440311/41.
XX	
PS	New disclosure; SEQ ID NO 2; 156pp; English.
CC	The invention describes a new recombinant Equine Herpes Virus (EHV) where
CC	the protein GM is absent, and the EHV is free of heterologous elements.
CC	Also described are: a nucleic acid coding for an EHV defined above; a
CC	vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC	recombinant EHV; and a cell line for use in the method, where the gene
CC	encoding the protein GM is transfected into the cell line, and the cell
CC	line expresses GM. The vaccine comprising the EHV or nucleic acid
CC	encoding EHV is useful for treating and/or preventing EHV-associated
CC	condition, and for monitoring the therapeutic success. The recombinant
CC	EHV is useful as a vaccine against EHV infections. This sequence
CC	represents an Equine herpesvirus 4 genome in which nucleotides 92681-
CC	92731 and 93765-93865, comprising regions of the GM gene, have been
CC	deleted.
XX	
SQ	Sequence 145444 BP; 36178 A; 36893 C; 36497 G; 35876 T; 0 U; 0 Other;
	Query Match 5.4%; Score 37.8; DB 12; Length 145444;
	Best Local Similarity 61.9%; Pred. No. 4;
	Matches 60; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
OY	230 TAGCGGAACGGCATGTTTTCGCCAGACTGCCTATGACATGTAAAGACCACCGTTTG 289
Dd	46820 TTGACGATCTGCCATGTTTTGGCACAACGACGATCTACCTGGCGGCCCAATATAG 46761
OY	290 GCCTTAACGATCGTTTAAACCGCGATTATACGACC 326
Dd	46760 GACTAAGAACGACCTTCCCCCGCGGTTTATGAGCC 46724
	RESULT 10
ID	ADP74202/C
ID	ADP74202 standard; DNA; 145596 BP.
XX	
AC	ADP74202;
XX	
DT	26-AUG-2004 (first entry)
XX	
DE	Equine herpesvirus 4 genome seqid 2.
KW	virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;
KW	EHV-associated condition; Equine herpesvirus 4; EHV4; ds.
XX	
OS	Equine herpesvirus 4.
XX	
PX	US2004109873-A1.

XX	10-JUN-2004.
XX	
PF	21-JUL-2003; 2003US-00624149.
XX	
PR	19-JUL-2002; 2002DE-01033064.
PR	14-AUG-2002; 2002US-0403282P.
PR	11-APR-2003; 2003DE-01017008.
XX	(BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
PA	New recombinant equine herpes (EHV) virus free of heterologous elements,
PI	and where protein GM has been deleted, useful as a vaccine for treating
PT	or preventing EHV infections.
XX	
PS	Disclosure; SEQ ID NO 2; 156pp; English.
XX	
CC	The invention describes a new recombinant Equine Herpes Virus (EHV) where
CC	the protein GM is absent, and the EHV is free of heterologous elements.
CC	Also described are: a nucleic acid coding for an EHV defined above; a
CC	vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC	recombinant EHV; and a cell line for use in the method, where the gene
CC	encoding the protein GM is transfected into the cell line, and the cell
CC	line expresses GM. The vaccine comprising the EHV or nucleic acid
CC	encoding EHV is useful for treating and/or preventing EHV-associated
CC	condition, and for monitoring the therapeutic success. The recombinant
CC	EHV is useful as a vaccine against EHV infections. This sequence
CC	represents the Equine herpesvirus 4 genome.
XX	
SQ	Sequence 145596 BP; 36213 A; 36932 C; 36529 G; 35922 T; 0 U; 0 Other;
	Query Match 5.4%; Score 37.8; DB 12; Length 145596;
	Best Local Similarity 61.9%; Pred. No. 4;
	Matches 60; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
OY	230 TAGCGGAACGGCATGTTTTCGCCAGACTGCCTATGACATGTAAAGACCACCGTTTG 289
Dd	46820 TTGACGATCTGCCATGTTTTGGCACAACGACGATCTACCTGGCGGCCCAATATAG 46761
OY	290 GCCTTAACGATCGTTTAAACCGCGATTATACGACC 326
Dd	46760 GACTAAGAACGACCTTCCCCCGCGGTTTATGAGCC 46724
	RESULT 11
ID	AHH24065
ID	AHH24065 standard; DNA; 4590 BP.
XX	
AC	AHH24065;
XX	
DT	29-AUG-2001 (first entry)
XX	
DE	Yeast AOD9604-associated DNA sequence, SEQ ID NO:1.
XX	
KW	Human growth hormone analogue peptide; hGH; AOD9604; lipid metabolism;
KW	modulation; lipolysis stimulation; hormone-sensitive lipase stimulation;
KW	lipogenesis inhibition; acetyl CoA carboxylase inhibition; obesity;
KW	functional food; transgenic yeast; fat/lean ratio; food use; ds.
XX	
OS	Saccharomyces cerevisiae.
XX	
FH	Key Location/Qualifiers
FT	misc_feature 10
FT	/tag= a
FT	/note= "Represented as * in the specification"
FT	misc_feature 3617
FT	/tag= b
FT	/note= "Represented as * in the specification"
FT	misc feature 3649

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.

P-PSDB; ABU40120.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 31860; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <http://wipo.int/pub/published/pct/sequences>

Sequence 711 BP; 120 A; 161 C; 304 G; 126 T; 0 U; 0 Other;

Query Match 5.2%; Score 37; DB 8; Length 711;
Best Local Similarity 47.3%; Pred. No. 0.72;

428	CGTTGGCGTTTTCGGGATCATCCCGGCAACACCCGCCACTCAACGACGTCGGGATCGG	487
a		
400	CGTTTCGGGCACCATGGCACCGCGGCCACCACTTCCACCAACCGTGGCCACCAACCAC	341
b		
488	TTGGACAAAGCAACACGTTGGTCTCGGGGTCTTCTGGACAAACACGCAACAGGGGAC	547
y		
340	CGCGGCTTTCACCAACACCGCTGGCCACCGCCACCGCCGCTTCCACCAACCGTCGACCA	281
b		
548	AGTCAAGCACTGTGCAGCCAAACACCGGATCACCGCCCGCGGCCAAAGCGCTGCCACAGT	607
y		
280	CGCCACCGCGGCTTCCACCGCCACCGTGGCCACCGCGCGCGCTTCCACCGCCACCGT	221
b		
608	CTACCCCGCCGCCCAACCCAAAATACCCCCAAGGGGGTTAAGGACAGACCTTTGTGCAC	664
y		
220	GGCCACCGCGCGCCCACTTCCACCGCCACCGTGGCCACCGCCACCGCCACCGCCACCG	164
b		

RESULT 13

AAI99682 27

Continuation (28 of 45) of AA199682 from base 2700001 (Mycobacterium tuberculosis strain H37Rv)
 WP Sequence split into 45 fragments LOCUS AA199682 Accession AA199682

WP	Fragment Name	Begin	End
WP	AA199682_00	100001	1100000
WP	AA199682_01	100001	2100000
WP	AA199682_02	200001	3100000
WP	AA199682_03	300001	4100000
WP	AA199682_04	400001	5100000
WP	AA199682_05	500001	6100000
WP	AA199682_06	600001	7100000
WP	AA199682_07	700001	8100000
WP	AA199682_08	800001	9100000
WP	AA199682_09	900001	10100000
WP	AA199682_10	1000001	11100000
WP	AA199682_11	1100001	12100000
WP	AA199682_12	1200001	13100000
WP	AA199682_13	1300001	14100000
WP	AA199682_14	1400001	15100000
WP	AA199682_15	1500001	16100000
WP	AA199682_16	1600001	17100000
WP	AA199682_17	1700001	18100000
WP	AA199682_18	1800001	19100000
WP	AA199682_19	1900001	20100000
WP	AA199682_20	2000001	21100000
WP	AA199682_21	2100001	22100000
WP	AA199682_22	2200001	23100000
WP	AA199682_23	2300001	24100000
WP	AA199682_24	2400001	25100000
WP	AA199682_25	2500001	26100000
WP	AA199682_26	2600001	27100000
WP	AA199682_27	2700001	28100000
WP	AA199682_28	2800001	29100000
WP	AA199682_29	2900001	30100000
WP	AA199682_30	3000001	31100000
WP	AA199682_31	3100001	32100000
WP	AA199682_32	3200001	33100000
WP	AA199682_33	3300001	34100000
WP	AA199682_34	3400001	35100000
WP	AA199682_35	3500001	36100000
WP	AA199682_36	3600001	37100000
WP	AA199682_37	3700001	38100000
WP	AA199682_38	3800001	39100000
WP	AA199682_39	3900001	40100000
WP	AA199682_40	4000001	41100000
WP	AA199682_41	4100001	42100000
WP	AA199682_42	4200001	43100000
WP	AA199682_43	4300001	44100000
WP	AA199682_44	4400001	4411529

Query Match 5.1%: Score 36.2; DB 4; Length 110000;

Query Match	5.1%	Score	10.0000
Best Local Similarity	45.6%	Pred. No. 11	
Matches 128; Conservative	0	Mismatches 153;	Indels 0; Gaps 0

Qy	397	GCCGATCAGTCTGCTTTTACACAGCCGCGCGTGGTGGTTCGGGATCATCCCGCNA	456
Db	105126	GCGACCGGCAGACACCCCGCGCGCCACGCGCGGTTTCGCGCGGCACCGCATTG	105185
Qy	457	CACCCCCCACTCAAACGAGCTCGGCATCCGTTGGACAACAGCAACACGTGTGTCGGG	516
Db	105186	CCGCGGCGCGCGTCAACCGCGCGCGGAGATACCGGCGGCCATTTATTCCGGTA	105245
Qy	517	TCCTTGTGACACAAACCGCAACAGGAGACACAGTCAAGCATGTCCAGCGCAACACCGGA	576
Db	105246	GCCCGGCACCGCGGCACCGCGCGCGCACCGGCACACCGGCCCGCCACACCGCA	105305
Qy	577	TCACGCGCGCGGCCAAGCGGTGCCACAGTCTACCCCGCCCCCAACCCAAATACCCCC	636
Db	105306	ACGCCACGGGCGCGCTTGTTACGAGAGCCACCCTCCCGACACCGTTGCGGCCACC	105365
Qy	637	CAGGGGGGTAGGGAACAGACTTCTGTCAACACGGGACAATC	677
Db	105366	CCACCGGCACCGCATCGCCCCGTTCGACCGCTGCCAAACC	105406

RESULT 14

AAI199682_28
Continuation (29 of 45) of AAI199682 from base 2800001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AAI199682 Accession Aai199682
WP Fragment Name Begin End
WP AAI199682_00 1 110000
WP AAI199682_01 100001 210000
WP AAI199682_02 200001 310000
WP AAI199682_03 300001 410000
WP AAI199682_04 400001 510000
WP AAI199682_05 500001 610000
WP AAI199682_06 600001 710000
WP AAI199682_07 700001 810000
WP AAI199682_08 800001 910000
WP AAI199682_09 900001 1010000
WP AAI199682_10 1000001 1110000
WP AAI199682_11 1100001 1210000
WP AAI199682_12 1200001 1310000
WP AAI199682_13 1300001 1410000
WP AAI199682_14 1400001 1510000
WP AAI199682_15 1500001 1610000
WP AAI199682_16 1600001 1710000
WP AAI199682_17 1700001 1810000
WP AAI199682_18 1800001 1910000
WP AAI199682_19 1900001 2010000
WP AAI199682_20 2000001 2110000
WP AAI199682_21 2100001 2210000
WP AAI199682_22 2200001 2310000
WP AAI199682_23 2300001 2410000
WP AAI199682_24 2400001 2510000
WP AAI199682_25 2500001 2610000
WP AAI199682_26 2600001 2710000
WP AAI199682_27 2700001 2810000
WP AAI199682_28 2800001 2910000
WP AAI199682_29 2900001 3010000
WP AAI199682_30 3000001 3110000
WP AAI199682_31 3100001 3210000
WP AAI199682_32 3200001 3310000
WP AAI199682_33 3300001 3410000
WP AAI199682_34 3400001 3510000
WP AAI199682_35 3500001 3610000
WP AAI199682_36 3600001 3710000
WP AAI199682_37 3700001 3810000
WP AAI199682_38 3800001 3910000
WP AAI199682_39 3900001 4010000
WP AAI199682_40 4000001 4110000
WP AAI199682_41 4100001 4210000
WP AAI199682_42 4200001 4310000
WP AAI199682_43 4300001 4410000
WP AAI199682_44 4400001 4411529

Query Match 5.1%; Score 36.2; DB 4; Length 110000;
Best Local Similarity 45.6%; Pred. No. 11;
Matches 128; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
QY 397 GCCGATCAGTCTGCTTTACACAGCCGCGGTTGGCGTTTTCGGGATCATCCCGCAA 456
DB 5126 GCCGACCCGCCAGCACCCCGCGCGCCACGCGCGTTTCCGCGCGCACCGCATTTG 5185
QY 457 CACCCCGGACCTCAACAGCGTGGCATCCGTTGGACACAGACAGTGTGTGCGGG 516
DB 5186 CCGCGCGCGCGCGCGTCCACCGCGCGCGCGAGATACCGCGCGCGCCATTATTATTCGGGTA 5245
QY 517 TCTTCTGGACAAACACCGGAGACAGTCAAGCAGTGTCCAGGCAACAAACCGGA 576
DB 5246 GCCCGGACCCCGCGGACCGCGCGGACCGGACACCGCGCGCGCGCGGACCGGCA 5305
QY 577 TCACCGCGCGCGCGGCGGAGCGTGCACAGTCTACCGCGCGCGCGGCGGCGGCGGCGG 636
DB 5306 AGCCACCGCGCGCGCGGTTACCGAGAGCCACCTCCCGGACCGCGTGTGCGCGCAC 5365
QY 637 CAGGGGGGTAAGGGACAGACCTTGTTCACACCGGACATC 677
DB 5366 CCACCGGACCGGCGGATCGCGCGCGCGTCCGACCGGCGGCGGCGGCGGCGGCGG 5406

RESULT 15

AAI199683_27
Continuation (28 of 44) of AAI199683 from base 2700001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AAI199683 Accession Aai199683
WP Fragment Name Begin End
WP AAI199683_00 1 110000
WP AAI199683_01 100001 210000
WP AAI199683_02 200001 310000
WP AAI199683_03 300001 410000
WP AAI199683_04 400001 510000
WP AAI199683_05 500001 610000
WP AAI199683_06 600001 710000
WP AAI199683_07 700001 810000
WP AAI199683_08 800001 910000
WP AAI199683_09 900001 1010000
WP AAI199683_10 1000001 1110000
WP AAI199683_11 1100001 1210000
WP AAI199683_12 1200001 1310000
WP AAI199683_13 1300001 1410000
WP AAI199683_14 1400001 1510000
WP AAI199683_15 1500001 1610000
WP AAI199683_16 1600001 1710000
WP AAI199683_17 1700001 1810000
WP AAI199683_18 1800001 1910000
WP AAI199683_19 1900001 2010000
WP AAI199683_20 2000001 2110000
WP AAI199683_21 2100001 2210000
WP AAI199683_22 2200001 2310000
WP AAI199683_23 2300001 2410000
WP AAI199683_24 2400001 2510000
WP AAI199683_25 2500001 2610000
WP AAI199683_26 2600001 2710000
WP AAI199683_27 2700001 2810000
WP AAI199683_28 2800001 2910000
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WP AAI199683_32 3200001 3310000
WP AAI199683_33 3300001 3410000
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WP AAI199683_36 3600001 3710000
WP AAI199683_37 3700001 3810000
WP AAI199683_38 3800001 3910000
WP AAI199683_39 3900001 4010000
WP AAI199683_40 4000001 4110000
WP AAI199683_41 4100001 4210000
WP AAI199683_42 4200001 4310000
WP AAI199683_43 4300001 4403765

Query Match 5.1%; Score 36.2; DB 4; Length 110000;
Best Local Similarity 45.6%; Pred. No. 11;
Matches 128; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
QY 397 GCCGATCAGTCTGCTTTACACAGCCGCGGTTGGCGTTTTCGGGATCATCCCGCAA 456
DB 100579 GCCGACCCGCCAGCACCCCGCGCGCCACGCGCGTTTCCGCGCGCACCGCATTTG 100638
QY 457 CACCCCGGACCTCAACAGCGTGGCATCCGTTGGACACAGACAGTGTGTGCGGG 516
DB 100639 CCGCGCGCGCGCGGTCACCGCGCGCGCGAGATACCGCGCGCGCCATTATTATTCGGGTA 100698
QY 517 TCTTCTGGACAAACACCGGAGACAGTCAAGCAGTGTCCAGGCAACAAACCGGA 576
DB 100699 GCCCGGACCCCGCGGACCGCGCGGACCGGACACCGCGCGCGCGGACCGGCA 100758
QY 577 TCACCGCGCGCGCGGCGGAGCGTGCACAGTCTACCGCGCGCGCGGCGGCGGCGGCGG 636
DB 100759 AGCCACCGCGCGCGCGTTCACCGAGAGCCACCTCCCGGACCGCGTGTGCGGCGCAC 100818
QY 637 CAGGGGGGTAAGGGACAGACCTTGTTCACACCGGACATC 677

Db 100819 CCACCGGACCGCCATCGCCCCCGTCCGACCCCTGCCAAACC 100859

Search completed: September 25, 2005, 21:51:41
Job time : 538 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2005, 21:30:54 ; Search time 3219 Seconds
(without alignments)
8336.536 Million cell updates/sec

Title: US-09-874-140-1
Perfect score: 705
Sequence: 1 atgacacacccgcatcgctc.....cttcaagaagtcgtagggtg 705

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_ges1: *
9: gb_ges2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45.6	6.5	434	9	CNS049AP
2	44.8	6.4	884	9	CNS006U0
3	44.4	6.3	1013	9	CNS016KT
4	42.8	6.1	970	9	CNS010C9
5	42.2	6.0	977	9	CNS000X7
6	41.8	5.9	1235	4	BM473847
7	40.8	5.8	710	9	AG135197
8	40.2	5.7	1156	9	AG075888
9	40.2	5.7	1201	9	CNS0169V
10	40	5.7	910	9	CNS006ON
11	39.6	5.6	454	9	CE497548
12	39.6	5.6	1055	8	BZ144309
13	39.4	5.6	870	9	AG471975
14	39.4	5.6	922	9	CNS0073W
15	39.2	5.6	787	9	CC910437
16	39.2	5.6	942	6	CB314169
17	39.2	5.6	1537	5	BU372422
18	39	5.5	696	8	BZ365757
19	39	5.5	970	1	AL519510
20	38.4	5.4	961	9	AL098641
21	38.4	5.4	1606	4	BG027840
22	38.2	5.4	600	8	BZ895383
23	38.2	5.4	1101	9	CNS00KK2
24	38	5.4	529	9	CNS00LHZ

C 25	38	5.4	602	1	AI727059	BNLGH1724
C 26	38	5.4	752	7	C0096155	CO096155 GR_Eal9D
C 27	38	5.4	804	7	CO107101	CO107101 GR_Eb003
C 28	38	5.4	806	9	AG081452	AG081452 Pan trogl
C 29	38	5.4	808	7	CO118443	CO118443 GR_Eb020
C 30	38	5.4	815	7	CO123895	CO123895 GR_Eb06G
C 31	37.8	5.4	392	1	AI397669	AI397669 NCSC5H5T3
C 32	37.8	5.4	623	7	CF421899	CF421899 NCST3d87
C 33	37.8	5.4	841	9	AG388909	AG388909 Mus muscu
C 34	37.8	5.4	869	5	BU959836	BU959836 AGENCOURT
C 35	37.8	5.4	878	4	BG034409	BG034409 602302810
C 36	37.8	5.4	939	9	CNS00CNG	AL059400 Drosophil
C 37	37.6	5.3	936	9	CNS01608	AL106130 Drosophil
C 38	37.4	5.3	636	7	CO080152	CO080152 GR_Ea43G
C 39	37.4	5.3	936	5	BU151687	BU151687 AGENCOURT
C 40	37.4	5.3	1097	7	CK212140	CK212140 FGAS02400
C 41	37.4	5.3	1473	9	CL972108	CL972108 OeIFCC041
C 42	37.2	5.3	410	1	AU298532	AU298532 Drosophil
C 43	37.2	5.3	909	9	CNS00JTL	AL076720 Drosophil
C 44	37.2	5.3	953	9	CNS017Y4	AL108646 Drosophil
C 45	37.2	5.3	964	9	CNS003WG	AL065254 Drosophil

ALIGNMENTS

RESULT 1	CNS049AP	434 bp	DNA	linear	GSS 01-SEP-2000
LOCUS	Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone				
DEFINITION	093G05 of library G from Tetraodon nigroviridis, genomic survey sequence.				
ACCESSION	AL280330				
VERSION	AL280330.1	GI:8018616			
KEYWORDS	GSS: genome survey sequence.				
SOURCE	Tetraodon nigroviridis				
ORGANISM	Tetraodon nigroviridis				
REFERENCE	1 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.				
AUTHORS	Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence				
TITLE	Nat. Genet. 25 (2), 235-238 (2000)				
JOURNAL	20296633				
MEDLINE	10835645				
PUBMED	2				
REFERENCE	2 Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.				
AUTHORS	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis				
TITLE	Genome Res. 10 (7), 939-949 (2000)				
JOURNAL	20359837				
MEDLINE	10899143				
PUBMED	3 (bases 1 to 434)				
REFERENCE	Genoscope.				
AUTHORS	Direct Submission				
TITLE	Submitted (12-APR-2000) Genoscope - Centre National de Sequençage :				
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr)				
FEATURES	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.				
source	Location/Qualifiers				
	1..434				
	/organism="Tetraodon nigroviridis"				
	/mol_type="genomic DNA"				

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/db_xref="taxon:99883"
/clone="093005"
/clone_lib="G"
/note="Genoscope sequence ID : COBG093AD03SP1-end :
PUC-Ori"

ORIGIN
Query Match          6.5%; Score 45.6; DB 9; Length 434;
Best Local Similarity 41.9%; Pred. No. 0.03;
Matches 96; Conservative 24; Mismatches 109; Indels 0; Gaps 0;

QY 409 GTTTACACAGCCCGCTGGCGTTTTCGGGATCATCCCGCAACACCCCACT 468
      ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 72 GCTGAGCGGACCGGNTCCGTCGTCGCGCATMASWCGCGAGCAGCCTCAGCT 131
      ||| | | | | | | | | | | | | | | | | | | | | | | | |

QY 469 CAAACGAGTCGGCATCCGTTGGACACAGCAGCAGCTGTCGGGGTCTTCTGGACAA 528
      ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 132 CCATCGTCGTCGCCGCTCASMGGCGSAGAGCCGCGCTCCMTCGYCSYCACGGCCA 191
      ||| | | | | | | | | | | | | | | | | | | | | | | | |

QY 529 CAACGCAACAGGAGCAGCAGTCAAGCACTGTCCAGCAACAAACGGATCAGCGCCGCG 588
      ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 192 YCAGAGCCGAGCGCGMGAMCCCGCGGCTCCGTCGTCGCCGCCGCCCAACAGCGCGAG 251
      ||| | | | | | | | | | | | | | | | | | | | | | | | |

QY 589 GCCCAAGCGGTGCCAGCTTACCCCGCCCGCCCAACCAAAATACCCCCC 637
      ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 252 AMSCCCCCGCTCCAYCSYCCCGCGCGCCGCCGCCGCCGCCGCCGCCGCCGCC 300
      ||| | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
CNS006U0/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14N21 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL065923
AL065923.1 GI:4944891
GSS.
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 884)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoler in Pister de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
1..884
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14N21"
/clone_lib="RPCI-98"
/note="end : T7"

ORIGIN

Query Match          6.3%; Score 44.4; DB 9; Length 1013;
Best Local Similarity 18.7%; Pred. No. 0.062;
Matches 75; Conservative 141; Mismatches 185; Indels 0; Gaps 0;

QY 294 AAAACGTAGTTTAACCCGCGTATTATAGGACCACAAACCCCAATCCATCAGGTTT 353
      :::: : : : : : : : : : : : : : : : : : : : : : : : :
Db 880 MMVMNMHTTKKKKTKTHMVMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNM 821
      :::: : : : : : : : : : : : : : : : : : : : : : : : :
QY 354 GGAATCTCGGGCGCTACTATTTCGCAAAAAACAGAGCGCGGATCAGTCTGCTTT 413
      ::: : : : : : : : : : : : : : : : : : : : : : : : :
Db 820 MNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNM 761
      ::: : : : : : : : : : : : : : : : : : : : : : : : :
QY 414 ACAACAGCCCGCGGCTTGGCGTTTTCGGGATCATCCCGCAACACCCCACTCAAC 473
      :::: : : : : : : : : : : : : : : : : : : : : : : :
Db 760 CMMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNM 701
      :::: : : : : : : : : : : : : : : : : : : : : : : :
QY 474 GACGTGCGGATCCGTTGGACACAGCAACAGTGTGTCGGGGTCTTCTGGACACAA 533
      : : : : : : : : : : : : : : : : : : : : : : : : :
Db 700 MAMCMCMCMCMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNMNM 641
      : : : : : : : : : : : : : : : : : : : : : : : : :
QY 534 GCAACAGGAGGACAGTCAAGCACTGTCCAGCAACAAACCGGATCAGCGCCGCG 593
      : : : : : : : : : : : : : : : : : : : : : : : : :
Db 640 CCCCCMNMMAACAAACAAAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAM 581
      : : : : : : : : : : : : : : : : : : : : : : : : :
QY 594 AGGCGTGCACAGTCTACCCCGCCCGCCCAACCAAAATACCCCGGGGGTAAAGG 653
      : : : : : : : : : : : : : : : : : : : : : : : : :
Db 580 MCTCACCAAMCAAHMAAAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAM 521
      : : : : : : : : : : : : : : : : : : : : : : : : :
QY 654 GACCTTGTCAACAGGAGACATCTGGAAACGCTTCAAGAA 694
      : : : : : : : : : : : : : : : : : : : : : : : : :
Db 520 BMCYBCCCCCMMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAM 480
      : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
CNS016KT
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN16J16 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106871
AL106871.1 GI:5624218
GSS.
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1013)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (DrosBAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
Location/Qualifiers
1..1013
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN16J16"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"

ORIGIN

Query Match          6.3%; Score 44.4; DB 9; Length 1013;
```



```

Best Local Similarity 15.0%; Pred. No. 0.084;
Matches 37; Conservative 93; Mismatches 116; Indels 0; Gaps 0;

Qy 415 CAACAGCCCGCGCGTGGCGTGTTCGGGATCATCCCGCGCAACACCCCGCCACCTCAAACG 474
    | : : : | | : : : | | : : : | : : : | : : : | : : : | : : : | : : :
Db 246 CMTWMSCCCNWNCWMSGSCCCSCHSMGMMCMWMMCMCMWMMWMMWMMWMMWMMWMMWMMWMM 305
    | : : : | | : : : | | : : : | : : : | : : : | : : : | : : : | : : :
Qy 475 ACGTCGGGATCCGTTGGACAACAGCAACACGATGTCGCGGTCTTCTTGGAACAACACCG 534
    | : : : | | : : : | | : : : | : : : | : : : | : : : | : : : | : : :
Db 306 AMCTGNTNTNGMGTTHMMNGTNTTMMGNGMNGMNGMNNNCGMNNNNMMWMMWMMWMMWMM 365
    | : : : | | : : : | | : : : | : : : | : : : | : : : | : : : | : : :
Qy 535 CAACAGGAGGACAGTCAAGCACTGTCAGGCAACACCGGATCACCGCCCGCGGCCCAA 594
    | : : : | | : : : | | : : : | : : : | : : : | : : : | : : : | : : :
Db 366 GMGCMGGGMMGMWNTCTTGMGMCMNMCMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMM 425
    | : : : | | : : : | | : : : | : : : | : : : | : : : | : : : | : : :
Qy 595 GGCCTGCACAGTCTACCCCGCCCGCCCAACCCAAATACCCCGCGGGGGTGAAGGACAG 654
    | : : : | | : : : | | : : : | : : : | : : : | : : : | : : : | : : :
Db 426 TMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMM 485
    | : : : | | : : : | | : : : | : : : | : : : | : : : | : : : | : : :
Qy 655 ACCTTG 660
    | : : |
Db 486 GTCTYG 491
    | : : |

RESULT 4
CNS010C9/c
LOCUS
DEFINITION
  CNS010C9 970 bp DNA linear GSS 26-JUL-1999
  Drosophila melanogaster genome survey sequence Sp6 end of BAC
  BACN03L05 of DrosBAC library from Drosophila melanogaster (fruit
  fly), genomic survey sequence.
ACCESSION
  AL098787 GI:5610398
VERSION
  AL098787.1 GSS.
KEYWORDS
  GSS.
SOURCE
  Drosophila melanogaster (fruit fly)
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 970)
  Genoscope.
  Direct Submission
  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
  BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
  - web : www.genoscope.cns.fr)
  Determination of this BAC-end sequence was carried out as part of a
  collaboration with the European Drosophila Genome Project (EDGP) -
  http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
  library (Dros BAC) was made by Alain Billaud at CEPH (Centre
  d'Etude du Polymorphisme Humain) with funding provided by a MRC
  project grant. The DNA was prepared from embryos by Alain Bucheton
  and Genevieve Payan. It has been constructed in the vector
  pBelobAC11.
FEATURES
    Location/Qualifiers
        1..970
            /organism="Drosophila melanogaster"
            /mol_type="genomic DNA"
            /db_xref="taxon:7227"
            /clone="BACN03L05"
            /clone_lib="DrosBAC"
            /plasmid="pBelobAC11"
            /note="end : Sp6"

Query Match
Best Local Similarity 6.1%; Score 42.8; DB 9; Length 970;
Matches 42; Conservative 77; Mismatches 63; Indels 0; Gaps 0;

Qy 463 CCACCTCAAACGAGTCGCGCATCCGTTGGACAACAGCAACACGTCGTGCGGGTCTTCT 522
    | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 922 SMSVMCSVSSRSSVARAVASVCSRRSSMSRAVARVARGACASASRSVRVVRARAG 863
    | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Qy 523 GGACACAACCGCAAGGGAGCAAGTCAAGCACTGTCAGGCAACACCGGATCACCG 582
    | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :

```



```
VERSION AG075888.1 GI:16627690
SOURCE GSS.
ORGANISM Pan troglodytes (chimpanzee)

REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
          Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
          Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
          1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
          (E-mail: chimpanzee@riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
          Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end
          was generated during the R&D process and may have higher chance of
          clone tracking errors.
          PRIMERS
          Sequencing: M13Rev
          LIBRARY
          Vector : pKS145
          R.Site 1 : SacI
          R.Site 2 : SacI
          Location/Qualifiers
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              /db_xref="taxon:9598"
              /clone="PTB-068020.R"
              /sex="male"
              /cell_type="lymphoblast"
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ORIGIN
Query Match 5.7%; Score 40.2; DB 9; Length 1156;
Best Local Similarity 50.8%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 93;

QY 449 CCCCACACACCCACCTCAAAGAGCGTCGGCATCGGTGGACAAACAGCAACACGTGG 508
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Db 328 CCGCGCCACACCGGACACAGACCCCGCGAGCTCCCGCGCGCGCGCGCGCGCG 387

QY 509 TGTGGGGTCTTTGGACAAACCGCAACAGGAGCAGTCAAGTCAAGTCAAGTCAAG 568
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Db 388 AGCCGGCAGCGCACCAGCAACAGCCCGCAGACCCCGCGCAATCCGCGCGCGCCAA 447

QY 569 CAACCGGATCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 628
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Db 448 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 507

QY 629 ATACCCCCC 637
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Db 508 GTGACCCCC 516

RESULT 9
CNS0169V 1201 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BAC15C06 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL106477
VERSION AL106477.1 GI:5622081
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CNS0169V 910 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BAC14J21 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL065629
VERSION AL065629.1 GI:4944698
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
          Ephydroidea; Drosophilidae; Drosophila.
          1 (bases 1 to 910)
          Direct Submission
          Genoscope.
          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
          - Web : www.genoscope.cns.fr)
          Determination of this BAC-end sequence was carried out as part of a

REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
          Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
          Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1999) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
          - Web : www.genoscope.cns.fr)
          Determination of this BAC-end sequence was carried out as part of a
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Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/orderinginformation.htm>). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 462 row: F Column: 7
Seq primer: SP6
Class: BAC ends.

FEATURES

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/strain="BN/SSNHsd/MCW"
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/sex="Female"
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/notice=vector: pTRABAC1.3; Site 1: MboI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong

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ORIGIN

Query Match	5.6%;	Score 39.6;	DB 8;	Length 1055;
Best Local Similarity	48.6%;	Prod. No. 2.3;		
Matches 108;	Conservative 0;	Mismatches 114;	Indels 0;	Gaps 0
Qy	406	TCTGCTTTTACAAACAGCCGCGCGTGTGGCGTTTCGGATCATCTCCCGCAACACCCGCCA	465	
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Qy	466	CCTCAAACGACGTGGGCATCCGTTGGACAACAGCAACACGTGGTGTGGGGGTCTTCTGGA	525	
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Qy	526	CAACAAACCGCAACAGGGAGCACAGTCAAGCAGTCCAGGCCAAACCGATCAACGCCCC	585	
Db	634	TCATCACCAACCAACCAATCATCATCACCAACCAATCACCATCATCATCATCATCAACCA	693	
Qy	586	CGGCCCCAAGCGTGCCACAGTCTTACCCCGCCCCCAACCCAA	627	
Db	694	CCACCAACCAACCAACCAACCAATCATCATCATCACCAACCAACCA	735	

RESULT 13

AG471975/c	AG471975	870 bp	DNA	linear	GSS 04-JUN-2004
LOCUS	Mus musculus molossinus DNA, clone:MSMg01-363u02.TJ, genomic survey				
DEFINITION	sequence.				
ACCESSION	AG471975				
VERSION	AG471975.1				
KEYWORDS	GSS.				
SOURCE	Mus musculus molossinus				
ORGANISM	Mus musculus molossinus				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.				
	1				
	BAC end Sequences of Library MSMg01				

2 (bases 1 to 870)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Title: Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@gsc.riken.jp, URL: <http://hgp.gsc.riken.go.jp/>,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSNg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center.
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

COMMENT

Information are derived from the mouse DNA library. For DNA library availability, please contact Kuniya Abe (abe@rtc.riken.jp) Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

PRIMERS

PRIMER : TJ
 Sequencing : TJ
 LIBRARY :
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.

FEATURES

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/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/db_xref="taxon:57486"
/db_xref="taxon:57486"
/clone="MSMG01-363J02.TJ"
/sex="male"
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clone_lib="MSMG01 Mouse Male BAC Library"
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ORIGIN

	Query Match	5.6%	Score 39.4;	DB 9;	Length 870;
	Best Local Similarity	44.6%;	Pred. No. 2.5;		
	Matches 115;	Conservative 0;	Mismatches 143;	Indels 0;	Gaps 0;
Qy	379	CCGCAAAAAACAGAGCGCGATCATGTCTGCTTTTACAACAGCGCCGCCGGTTCGGCGTTT	438		
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Qy	439	TGGGATCATCCCCGCAACACCCCACCACCTCAAACGACGTCGGCATCGGTTGGACACAG	498		
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Qy	499	CAACACGTGTGTGCGGGGTCTTCGGACAAACAACCGAACAGGAGACACAGTCAAGCACT	558		
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Qy	559	GTCAGCAACACACCGGATCACCGCCCGGGGGCCAGGCGTGCCACAGTCTACCCCGCCC	618		
Db	326	ACNNCNCNNNGGGGAAAAAAGGGGGGGGGCCCCCGCCCCACACCAACNCCACGGCCCC	267		
Qy	619	CCAACCCAAATACCCCC	636		
Db	266	CCCCCAACACACCCAC	249		

RESULT 14

CNS0073W/c	CNS0073W	922 bp	DNA	linear	GSS 03-JUN-1999
LOCUS	Drosophila melanogaster genome survey sequence TET3 end of BAC #				
DEFINITION	BACR14D09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL066784				
VERSION	AL066784.1				
KEYWORDS	GI:4945247				
SOURCE	GSS.				
ORGANISM	Drosophila melanogaster (fruit fly)				
	Drosophila melanogaster				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
	1 (bases 1 to 922)				

REFERENCE
AUTHORS
Genoscope
I (Dabbs)

<p>Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : esqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)</p>	<p>Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the</p>
<p>GENOSCOPE TITLE JOURNAL</p>	<p>COMMENT</p>


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QY 361 TCGGGGCTTACTATATTGCGCAAAACACACAGAGCGCGATCAGTCTGCTTTTACAACAG 420
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QY 421 CCGCGCGGCTTGGCGTTTTCGGGATCATCCCGCAACACCCCGACCTCAACAGAGCTCG 480
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QY 661 TCACACACGGGCAATCTCGAAACGCTTCAAGAGTCTGTAGGGTG 705
Db 661 TCACACACGGGCAATCTCGAAACGCTTCAAGAGTCTGTAGGGTG 705
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RESULT 2

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US-09-661-596A-76/c
; Sequence 76, Application US/09661596A
; Patent No. 6528066
; GENERAL INFORMATION:
; APPLICANT: Santos, Richard
; APPLICANT: Santos, Richard
; TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE
; FILE REFERENCE: 140.0011 01.01
; CURRENT APPLICATION NUMBER: US/09/661,596A
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/153,779
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella zoster
US-09-661-596A-76
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Query Match 100.0%; Score 705; DB 4; Length 124884;
Best Local Similarity 100.0%; Pred. No. 1.7e-226;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGACACAACCCGCATCGTCTGCTGAGTCTTTGATCCAGCAACCCCAACCATTTTCG 60
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Db 43078 GTGGAAGCAATTGCGGCTTACACCCCGTGTCTTTAATACGACTTTTAAACGCCAGTGA 43019
QY 121 CTTTTCGAACCTGGTCAACGTTGGACATCGCTGTATGCCAAGATTTTACACCGTGGGA 180
Db 43018 CTTTTCGAACCTGGTCAACGTTGGACATCGCTGTATGCCAAGATTTTACACCGTGGGA 42959
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RESULT 3

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US-09-913-514-1/c
; Sequence 1, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAMACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine
; FILE REFERENCE: 0216-0454P
; CURRENT APPLICATION NUMBER: US/09/913,514
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(124884)
; OTHER INFORMATION: Dumas Strain
US-09-913-514-1
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Query Match 100.0%; Score 705; DB 4; Length 124884;
Best Local Similarity 100.0%; Pred. No. 1.7e-226;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGACACAACCCGCATCGTCTGCTGAGTCTTTGATCCAGCAACCCCAACCATTTTCG 60
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QY 61 GTGGAAGCAATTGCGGCTTACACCCCGTGTCTTTAATACGACTTTTAAACGCCAGTGA 120
Db 43078 GTGGAAGCAATTGCGGCTTACACCCCGTGTCTTTAATACGACTTTTAAACGCCAGTGA 43019
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RESULT 4
US-09-913-514-2/c
; Sequence 2, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAMACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccin
; FILE REFERENCE: 0216-0454P
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/913,514
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JF01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 125157
; TYPE: DNA
; ORGANISM: Varicella virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(125157)
; OTHER INFORMATION: Attenuated Oka strain
US-09-913-514-2

Query Match 99.8%; Score 703.4; DB 4; Length 125157;
Best Local Similarity 99.9%; Pred. No. 5.9e-226;
Matches 704; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 42513 CCACAGTCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 42454
Qy 661 TCACACAGCGGACAAATCTGGAACGCTTCAAGAGTCGTAGGGTG 705
Db 42453 TCACACAGCGGACAAATCTGGAACGCTTCAAGAGTCGTAGGGTG 42409

RESULT 5
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
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; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 5.1%; Score 36.2; DB 3; Length 4403765;
Best Local Similarity 45.6%; Pred. No. 11; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
QY 397 GCGATCAGTCTGCTTTTACAACAGCCCGCGGTGGCGTTTTCGGGATCATCCCGCAA 456
Db 2800579 GCGACCCGCCAGCACCCCGCGCGCCACCGCCGCTTTCGGCGGACCGCATTTG 2800638
QY 457 CACCCCCCACTTAAGACGCTGCGCATCGTTGGACAACAGCAACACGTGTGTGCGGG 516
Db 2800639 CGCGCGCGCGCGCTCACCGCGCGCGCGAGATACCGCGCGGCCATTATTTCGGTA 2800698
QY 517 TCTTCGGACACAACCGCAACAGGAGCACAGTCAAGCACTGTCCAGCAACACCGGA 576
Db 2800699 GCGCGGACCGCGCGCACCGCGCGCGCACCGGACCGCGCGCGCGCGCACCGCA 2800758
QY 577 TCACCGCGCGCGCGCGCAAGCGGTGCCACAGTCTACCGCGCGCGCGCAACCAAAATACCC 636
Db 2800759 AGCCACCGCGCGCGCGGTACCGAGAGCCACCTCCCGGACCGCTTTCGGCGCCAC 2800818
QY 637 CAGGGGGTAAGGACAGACCTTGTTCACACCGGGAATC 677
Db 2800819 CCACCGGCACCGCATCGCCCGCTCCGACCTGCCAAACC 2800859

RESULT 6

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
Query Match 5.1%; Score 36.2; DB 3; Length 4411529;
Best Local Similarity 45.6%; Pred. No. 11; Indels 0; Gaps 0;
Matches 128; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
QY 397 GCGATCAGTCTGCTTTTACAACAGCCCGCGGTGGCGTTTTCGGGATCATCCCGCAA 456
Db 2805126 GCGACCCGCCAGCACCCCGCGCGCCACCGCCGCTTTCGGCGGACCGCATTTG 2805185
QY 457 CACCCCCCACTTAAGACGCTGCGCATCGTTGGACAACAGCAACACGTGTGTGCGGG 516
Db 2805186 CGCGCGCGCGCGCTCACCGCGCGCGCGAGATACCGCGCGGCCATTATTTCGGTA 2805245
QY 517 TCTTCGGACACAACCGCAACAGGAGCACAGTCAAGCACTGTCCAGCAACACCGGA 576
Db 2805246 GCGCGGACCGCGCGCACCGCGCGCGCACCGGACCGCGCGCGCGCGCACCGCA 2805305
QY 577 TCACCGCGCGCGCGCAAGCGGTGCCACAGTCTACCGCGCGCGCGCAACCAAAATACCC 636
Db 2805306 AGCCACCGCGCGCGCGGTACCGAGAGCCACCTCCCGGACCGCTTTCGGCGCCAC 2805365
QY 637 CAGGGGGTAAGGACAGACCTTGTTCACACCGGGAATC 677

Db 2805366 CCACCGGCACCGCCATCGCCCCCGTCCGACCTGCCAAACC 2805406

RESULT 7

US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
Query Match 5.1%; Score 35.8; DB 3; Length 4403765;
Best Local Similarity 52.3%; Pred. No. 15;
Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 489 TGGACAACAGCAACGCTGGTGTGCGGGTCTTCTGGACAACACCGCAACCGGAGCACA 548
Db 1971184 TCGCGTCACTTCACTTCAGTGGCAGCTTGAACCAACCACTCAAGTTCAACGGGAATCA 1971125
QY 549 GTCAAGCACTGTCCAGCAACCAACCGGATCAACCGCGCGCGCGCAAGGCGTCCACAGTC 608
Db 1971124 CGCGCTTCACTTCAGTCCAGCTCGTGGCGGCGATCGACCATCGGCGCTCGCACCGCAGTC 608
QY 609 TACCGCGCGCGCAACCAACCAATACCCCGCAG 639
Db 1971064 AATTCCGCGCGCAATTCAACCGCGCGCTCGG 1971034

RESULT 8

US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
Query Match 5.1%; Score 35.8; DB 3; Length 4411529;
Best Local Similarity 52.3%; Pred. No. 15;
Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Db 175 CCGCAGCCGCTGTCTCATCCAGCGCTGTGAGCATCTGTTGGCACCGCCCGCCAGGCGC 234
QY 512 CGGGGTCTTCTGGACAACAAACCGCAACAGGGAGCACAGTCAAGCACTGTCCAGCCAAACAA 571
Db 235 CCGGGAGCAGCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 294
QY 572 CCGGATCACCGCCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 631
Db 295 AACCCGGACGCAAGCGCTCCACGGCGATCATCCAGGTGCGCGCGACAAACCCAAAGCGC 354
QY 632 CCGCCAGGGGGGTAAAGGACA 653
Db 355 ATCGCGTGGCGAATCGGTCA 376

RESULT 12

US-09-479-409-12
; Sequence 12, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-479-409-12

Query Match 4.8%; Score 34; DB 3; Length 642;

Best Local Similarity 48.0%; Pred. No. 0.56;

Matches 97; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 452 CGCAACACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 511
Db 175 CCGCAGCGCTGTCTCATCCAGCGCTGTGAGCATCTGTTGGCACCGCCCGCCAGGCGC 234
QY 512 CCGGGTCTTCTGGACAACAAACCGCAACAGGGAGCACAGTCAAGCACTGTCCAGCCAAACAA 571
Db 235 CCGGGAGCAGCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 294
QY 572 CCGGATCACCGCCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 631
Db 295 AACCCGGACGCAAGCGCTCCACGGCGATCATCCAGGTGCGCGCGACAAACCCAAAGCGC 354

QY 632 CCGCCAGGGGGGTAAAGGACA 653
Db 355 ATCGCGTGGCGAATCGGTCA 376

RESULT 13
US-09-479-453-12
; Sequence 12, Application US/09479453
; Patent No. 6313283
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,453
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-479-453-12

Query Match 4.8%; Score 34; DB 3; Length 642;

Best Local Similarity 48.0%; Pred. No. 0.56;

Matches 97; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 452 CGCAACACCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 511
Db 175 CCGCAGCGCTGTCTCATCCAGCGCTGTGAGCATCTGTTGGCACCGCCCGCCAGGCGC 234
QY 512 CCGGGTCTTCTGGACAACAAACCGCAACAGGGAGCACAGTCAAGCACTGTCCAGCCAAACAA 571
Db 235 CCGGGAGCAGCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 294
QY 572 CCGGATCACCGCCCGCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 631
Db 295 AACCCGGACGCAAGCGCTCCACGGCGATCATCCAGGTGCGCGCGACAAACCCAAAGCGC 354
QY 632 CCGCCAGGGGGGTAAAGGACA 653
Db 355 ATCGCGTGGCGAATCGGTCA 376

RESULT 14

US-08-911-853-29/c

; Sequence 29, Application US/08911853

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; Patent No. 6048710
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,853
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,092
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17612 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-911-853-29

Query Match 4.8%; Score 34; DB 3; Length 17612;
Best Local Similarity 48.0%; Pred.No.3.3;
Matches 97; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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Qy 572 CCGGATCACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 631
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Qy 632 CCCCCAGGGGGTAAGGACA 653
Db 3797 ATCGCGTGGGCGAATCGGTCA 3776

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; Sequence 29, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
```

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; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17612 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-479-409-29

Query Match 4.8%; Score 34; DB 3; Length 17612;
Best Local Similarity 48.0%; Pred.No.3.3;
Matches 97; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 452 CGCAACACCCCTCAACAGCAGCTCGGATCCGTTGGACACAGCAACACGTTGT 511
Db 3977 CGCAGCGCTGTCTCATCCAGCGCTGAGCATCTGTTGGACAGCCCGCGGCGG 3918

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2005, 22:52:03 ; Search time 676 Seconds
(without alignments)
6972.991 Million cell updates/sec

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Perfect score: 705
Sequence: 1 atgacaaacccatcgctc.....cttcaagaagtcgtagggtg 705

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Gapop 10.0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	705	100.0	124884	10	US-09-913-514-1
3	705	100.0	124884	16	US-10-288-823-76
4	703.4	99.8	125157	10	US-09-913-514-2
5	38	5.4	594	14	US-10-123-155-10
6	38	5.4	594	15	US-10-146-731-10
7	38	5.4	594	15	US-10-140-472-10

c	8	38	5.4	594	15	US-10-141-761-10	Sequence 10, Appl
c	9	38	5.4	594	16	US-10-142-885-10	Sequence 10, Appl
c	10	38	5.4	594	16	US-10-158-790-10	Sequence 10, Appl
c	11	38	5.4	594	17	US-10-137-871-10	Sequence 10, Appl
c	12	38	5.4	594	17	US-10-140-923-10	Sequence 10, Appl
c	13	38	5.4	594	17	US-10-141-756-10	Sequence 10, Appl
c	14	38	5.4	594	17	US-10-141-759-10	Sequence 10, Appl
c	15	38	5.4	594	17	US-10-140-805-10	Sequence 10, Appl
c	16	38	5.4	594	17	US-10-140-864-10	Sequence 10, Appl
c	17	38	5.4	594	18	US-10-142-426-10	Sequence 10, Appl
c	18	37.8	5.4	145597	19	US-10-624-149A-2	Sequence 2, Appli
c	19	37	5.2	711	17	US-10-282-122A-31860	Sequence 31860, A
c	20	36.6	5.2	573	19	US-10-437-963-9159	Sequence 9159, Ap
c	21	36.4	5.2	1049	14	US-10-123-155-358	Sequence 358, App
c	22	36.4	5.2	1049	15	US-10-146-731-358	Sequence 358, App
c	23	36.4	5.2	1049	15	US-10-140-472-358	Sequence 358, App
c	24	36.4	5.2	1049	15	US-10-141-761-358	Sequence 358, App
c	25	36.4	5.2	1049	16	US-10-142-885-358	Sequence 358, App
c	26	36.4	5.2	1049	16	US-10-158-790-358	Sequence 358, App
c	27	36.4	5.2	1049	17	US-10-137-871-358	Sequence 358, App
c	28	36.4	5.2	1049	17	US-10-140-923-358	Sequence 358, App
c	29	36.4	5.2	1049	17	US-10-141-756-358	Sequence 358, App
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c	31	36.4	5.2	1049	17	US-10-140-805-358	Sequence 358, App
c	32	36.4	5.2	1049	17	US-10-140-864-358	Sequence 358, App
c	33	36.4	5.2	1049	18	US-10-142-426-358	Sequence 358, App
c	34	36.2	5.1	843	19	US-10-437-963-98473	Sequence 98473, A
c	35	35.8	5.1	1383	17	US-10-282-122A-26326	Sequence 26326, A
c	36	35.8	5.1	1383	17	US-10-282-122A-28420	Sequence 28420, A
c	37	35.6	5.0	1222	20	US-10-335-053-193	Sequence 193, App
c	38	35.6	5.0	13416	15	US-10-205-032-11	Sequence 11, Appl
c	39	35.6	5.0	28874	22	US-10-915-740A-52	Sequence 52, Appl
c	40	35.6	5.0	60196	15	US-10-205-032-1	Sequence 1, Appli
c	41	35.6	5.0	2242716	22	US-10-915-740A-1068	Sequence 1068, Ap
c	42	35.4	5.0	646	20	US-10-363-345A-33541	Sequence 33541, A
c	43	35.4	5.0	646	20	US-10-363-345A-33542	Sequence 33542, A
c	44	35.4	5.0	646	21	US-10-363-483A-33541	Sequence 33541, A
c	45	35.4	5.0	646	21	US-10-363-483A-33542	Sequence 33542, A

ALIGNMENTS

RESULT 1

US-09-874-140-1

; Sequence 1, Application US/09874140

; Publication No. US20050202413A1

; GENERAL INFORMATION:

; APPLICANT: EICKMANN, Markus

; APPLICANT: GICKLHORN, Dorothee

; APPLICANT: RADSAK, Klaus

; APPLICANT: HAUSER, Hans-Peter

; APPLICANT: GISENDORF, Bernhard

; TITLE OF INVENTION: VARICELLA ZOSTER VIRUS (VZV) IMMUNOREACTIVE PROTEIN

; FILE REFERENCE: 058315/0127

; CURRENT APPLICATION NUMBER: US/09/874,140

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: US/09/219,337

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: DE 197 57 765.2

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 705

; TYPE: DNA

; ORGANISM: Varicella Zoster Virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(705)

US-09-874-140-1

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Query Match      100.0%; Score 705; DB 12; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.3e-229;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACACACACCGCATCGTCTGCTAGTCTTTGATCCAGCAACCCACACATTTTCG 60
DB 1 ATGACACACACCGCATCGTCTGCTAGTCTTTGATCCAGCAACCCACACATTTTCG 60

QY 61 GTGGAAGCAATTCGCGCTTACACCCCGTGTCTTAAATACGACTTTTAAACGCCAGTGA 120
DB 61 GTGGAAGCAATTCGCGCTTACACCCCGTGTCTTAAATACGACTTTTAAACGCCAGTGA 120

QY 121 CCTTTGCAACCTGGTCAACCGTGTGGACATCGCTGATGCCAGAAGCATTTTACACCGTGGGA 180
DB 121 CCTTTGCAACCTGGTCAACCGTGTGGACATCGCTGATGCCAGAAGCATTTTACACCGTGGGA 180

QY 181 GCCCGGCGCAGTGC CGCGGTGCGACGCTAACCATAATGCAAAATACGATACGCCGAACG 240
DB 181 GCCCGGCGCAGTGC CGCGGTGCGACGCTAACCATAATGCAAAATACGATACGCCGAACG 240

QY 241 GCATGTTTTCGCGAGACTGACCTTATGACATGTTTAAAGACCAACGTTGGCTTAAACCGT 300
DB 241 GCATGTTTTCGCGAGACTGACCTTATGACATGTTTAAAGACCAACGTTGGCTTAAACCGT 300

QY 301 ACGTTTAAACCCGCGTATTATACGACCAACACACCCCAAAATCCATCCATGAGTTTGGGAATC 360
DB 301 ACGTTTAAACCCGCGTATTATACGACCAACACACCCCAAAATCCATCCATGAGTTTGGGAATC 360

QY 361 TCGGGGCTTACTATATTGCGGCAAAAACACAGAGGCGCGATCAGTCTGCTTTTACAACG 420
DB 361 TCGGGGCTTACTATATTGCGGCAAAAACACAGAGGCGCGATCAGTCTGCTTTTACAACG 420

QY 421 CCGCGCGGCTTGGCGTTTTCGGGATCATCCCGCAACACACCCCACTCAAAACGACGTCG 480
DB 421 CCGCGCGGCTTGGCGTTTTCGGGATCATCCCGCAACACACCCCACTCAAAACGACGTCG 480

QY 481 GCATCCGTTGGACAACAGCAACACGCTGTGTGCGGGTCTTTTGGACAACACCGCAACAG 540
DB 481 GCATCCGTTGGACAACAGCAACACGCTGTGTGCGGGTCTTTTGGACAACACCGCAACAG 540

QY 541 GGAGCAGTCAAGCAGTGTTCAGCGCAACACCGGATCACCGCGCGCGGCCCAAGCGGTG 600
DB 541 GGAGCAGTCAAGCAGTGTTCAGCGCAACACCGGATCACCGCGCGCGGCCCAAGCGGTG 600

QY 601 CCACAGTCTACCCCGCCCAACCAAAATACCCCGAGGGGGTAAAGGACAGACCTTTG 660
DB 601 CCACAGTCTACCCCGCCCAACCAAAATACCCCGAGGGGGTAAAGGACAGACCTTTG 660

QY 661 TCACACAGGGACAATCTGGAACCGCTTCAAGAAGTCTGTAGGGTG 705
DB 661 TCACACAGGGACAATCTGGAACCGCTTCAAGAAGTCTGTAGGGTG 705

RESULT 2
US-09-913-514-1/c
; Sequence 1, Application US/09913514
; Publication No. US20030082210A1
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAWACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccin
; FILE REFERENCE: 0216-0454P
; CURRENT APPLICATION NUMBER: US/09/913,514
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
```

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; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(124884)
; OTHER INFORMATION: Dumas Strain
US-09-913-514-1

Query Match      100.0%; Score 705; DB 10; Length 124884;
Best Local Similarity 100.0%; Pred. No. 1e-228;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACACACACCGCATCGTCTGCTAGTCTTTGATCCAGCAACCCACACATTTTCG 60
DB 43138 ATGACACACACCGCATCGTCTGCTAGTCTTTGATCCAGCAACCCACACATTTTCG 43079

QY 61 GTGGAAGCAATTCGCGCTTACACCCCGTGTCTTAAATACGACTTTTAAACGCCAGTGA 120
DB 43078 GTGGAAGCAATTCGCGCTTACACCCCGTGTCTTAAATACGACTTTTAAACGCCAGTGA 43019

QY 121 CCTTTGCAACCTGGTCAACCGTGTGGACATCGCTGATGCCAGAAGCATTTTACACCGTGGGA 180
DB 43018 CCTTTGCAACCTGGTCAACCGTGTGGACATCGCTGATGCCAGAAGCATTTTACACCGTGGGA 42959

QY 181 GCCCGGCGCAGTGC CGCGGTGCGACGCTAACCATAATGCAAAATACGATACGCCGAACG 240
DB 42958 GCCCGGCGCAGTGC CGCGGTGCGACGCTAACCATAATGCAAAATACGATACGCCGAACG 42899

QY 241 GCATGTTTTCGCGAGACTGACCTTATGACATGTTTAAAGACCAACGTTGGCTTAAACCGT 300
DB 42898 GCATGTTTTCGCGAGACTGACCTTATGACATGTTTAAAGACCAACGTTGGCTTAAACCGT 42839

QY 301 ACGTTTAAACCCGCGTATTATACGACCAACACCCCAAAATCCATCCATGAGTTTGGGAATC 360
DB 42838 ACGTTTAAACCCGCGTATTATACGACCAACACCCCAAAATCCATCCATGAGTTTGGGAATC 42779

QY 361 TCGGGGCTTACTATATTGCGGCAAAAACACAGAGCGCGGATCAGTCTGCTTTTACAACAG 420
DB 42778 TCGGGGCTTACTATATTGCGGCAAAAACACAGAGCGCGGATCAGTCTGCTTTTACAACAG 42719

QY 421 CCGCGCGGCTTGGCGTTTTCGGGATCATCCCGCAACACCCCACTCAAAACGACGTCG 480
DB 42718 CCGCGCGGCTTGGCGTTTTCGGGATCATCCCGCAACACCCCACTCAAAACGACGTCG 42659

QY 481 GCATCCGTTGGACAACAGCAACACGCTGTGTGCGGGTCTTTTGGACAACACCGCAACAG 540
DB 42658 GCATCCGTTGGACAACAGCAACACGCTGTGTGCGGGTCTTTTGGACAACACCGCAACAG 42599

QY 541 GGAGCAGTCAAGCAGTGTTCAGCGCAACACCGGATCACCGCGCGCGGCCCAAGCGGTG 600
DB 42598 GGAGCAGTCAAGCAGTGTTCAGCGCAACACCGGATCACCGCGCGCGGCCCAAGCGGTG 42539

QY 601 CCACAGTCTACCCCGCCCAACCAAAATACCCCGAGGGGGTAAAGGACAGACCTTTG 660
DB 42538 CCACAGTCTACCCCGCCCAACCAAAATACCCCGAGGGGGTAAAGGACAGACCTTTG 42479

QY 661 TCACACAGGGACAATCTGGAACCGCTTCAAGAAGTCTGTAGGGTG 705
DB 42478 TCACACAGGGACAATCTGGAACCGCTTCAAGAAGTCTGTAGGGTG 42434

RESULT 3
US-10-288-823-76/c
; Sequence 76, Application US/10288823
; Publication No. US20030166168A1
; GENERAL INFORMATION:
; APPLICANT: Grose, Charles
; APPLICANT: Santos, Richard
; TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE
; FILE REFERENCE: 140.00110102
; CURRENT APPLICATION NUMBER: US/10/288,823
; CURRENT FILING DATE: 2002-11-06
```


; PRIOR APPLICATION NUMBER: US 09/661,596
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/153,779
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella zoster
US-10-288-823-76

Query Match 100.0%; Score 705; DB 16; Length 124884;
Best Local Similarity 100.0%; Pred. No. 1e-228;
Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACACACCCGATCGTCTGCTAGTCTTTGATCCAGCAACCCACACATTTTCG 60
DB 43138 ATGACACACCCGATCGTCTGCTAGTCTTTGATCCAGCAACCCACACATTTTCG 43079

QY 61 GTGGAAGCAATTCGCGCTTACACCCCGTTGCTTTAATACGACTTTTAAAGCCAGTGG 120
DB 43078 GTGGAAGCAATTCGCGCTTACACCCCGTTGCTTTAATACGACTTTTAAAGCCAGTGG 43019

QY 121 CCTTTGCAACCTGTCACCGTGTGACATCGCTGATGCCAGAGCATTTACACCGTGGGA 180
DB 43018 CCTTTGCAACCTGTCACCGTGTGACATCGCTGATGCCAGAGCATTTACACCGTGGGA 42959

QY 181 GCCGGCCGATGCGCGGTGCACCGCTAACCATATGCAATACGATACGCGCAACG 240
DB 42958 GCCGGCCGATGCGCGGTGCACCGCTAACCATATGCAATACGATACGCGCAACG 42899

QY 241 GCATGTTTGGCGAGACTGACCTATGACATGGTTAAGACCAACCGTTGGCTTAAACCGT 300
DB 42898 GCATGTTTGGCGAGACTGACCTATGACATGGTTAAGACCAACCGTTGGCTTAAACCGT 42839

QY 301 AGTTTAAACCCGCTATTATACGACACAAACCCCAATTCATTCATGAGTTTGGGAATC 360
DB 42838 AGTTTAAACCCGCTATTATACGACACAAACCCCAATTCATTCATGAGTTTGGGAATC 42779

QY 361 TCGGGGCTTACTATATTCGCGCAAAACACAGAGCGCGATCAGTCTGCTTTACACAG 420
DB 42778 TCGGGGCTTACTATATTCGCGCAAAACACAGAGCGCGATCAGTCTGCTTTACACAG 42719

QY 421 CCCGCGGCTTGGCGTTTTCGGGATCATCCCCGCAACACCCCGACCTCAAAACGACGTCG 480
DB 42718 CCCGCGGCTTGGCGTTTTCGGGATCATCCCCGCAACACCCCGACCTCAAAACGACGTCG 42659

QY 481 GCATCCGTTGGACAACAGCAACACGTCGTGTGCGGGTCTTCTGGACAACACCGCAACAG 540
DB 42658 GCATCCGTTGGACAACAGCAACACGTCGTGTGCGGGTCTTCTGGACAACACCGCAACAG 42599

QY 541 GGAGCACAGTCAAGCACTGTCAGCAACACCGGATCACCGCGCGCGCCCAAGCGTG 600
DB 42598 GGAGCACAGTCAAGCACTGTCAGCAACACCGGATCACCGCGCGCGCCCAAGCGTG 42539

QY 601 CCACAGTCTACCCCGCCCAACCAATATCCCGCAGGGGGTAAAGGACAGACCTTG 660
DB 42538 CCACAGTCTACCCCGCCCAACCAATATCCCGCAGGGGGTAAAGGACAGACCTTG 42479

QY 661 TCACACAGGGACAATCTGGAACGCTTCAAGAGTCTGAGGGTG 705
DB 42478 TCACACAGGGACAATCTGGAACGCTTCAAGAGTCTGAGGGTG 42434

RESULT 4

US-09-913-514-2/c
; Sequence 2, Application US/09913514
; Publication No. US20030082210A1
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAWACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki

; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine
; FILE REFERENCE: 0216-0454P
; CURRENT APPLICATION NUMBER: US/09/913,514
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 125157
; TYPE: DNA
; ORGANISM: Varicella virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(125157)
; OTHER INFORMATION: Attenuated Oka strain
US-09-913-514-2

Query Match 99.8%; Score 703.4; DB 10; Length 125157;
Best Local Similarity 99.9%; Pred. No. 3.5e-228;
Matches 704; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGACACACCCGATCGTCTGCTAGTCTTTGATCCAGCAACCCACACATTTTCG 60
DB 43113 ATGACACACCCGATCGTCTGCTAGTCTTTGATCCAGCAACCCACACATTTTCG 43054

QY 61 GTGGAAGCAATTCGCGCTTACACCCCGTTGCTTTAATACGACTTTTAAAGCCAGTGG 120
DB 43053 GTGGAAGCAATTCGCGCTTACACCCCGTTGCTTTAATACGACTTTTAAAGCCAGTGG 42994

QY 121 CCTTTGCAACCTGTCACCGTGTGACATCGCTGATGCCAGAGCATTTACACCGTGGGA 180
DB 42993 CCTTTGCAACCTGTCACCGTGTGACATCGCTGATGCCAGAGCATTTACACCGTGGGA 42934

QY 181 GCCGGCCGATGCGCGGTGCACCGCTAACCATATGCAATACGATACGCGCAACG 240
DB 42933 GCCGGCCGATGCGCGGTGCACCGCTAACCATATGCAATACGATACGCGCAACG 42874

QY 241 GCATGTTTGGCGAGACTGACCTATGACATGGTTAAGACCAACCGTTGGCTTAAACCGT 300
DB 42873 GCATGTTTGGCGAGACTGACCTATGACATGGTTAAGACCAACCGTTGGCTTAAACCGT 42814

QY 301 AGTTTAAACCCGCTATTATACGACCAACACCCCGACCTCAAAACGACGTCG 360
DB 42813 AGTTTAAACCCGCTATTATACGACCAACACCCCGACCTCAAAACGACGTCG 42754

QY 361 TCGGGGCTTACTATATTCGCGCAAAACACAGAGCGCGATCAGTCTGCTTTACACAG 420
DB 42753 TCGGGGCTTACTATATTCGCGCAAAACACAGAGCGCGATCAGTCTGCTTTACACAG 42694

QY 421 CCCGCGGCTTGGCGTTTTCGGGATCATCCCCGCAACACCCCGACCTCAAAACGACGTCG 480
DB 42693 CCCGCGGCTTGGCGTTTTCGGGATCATCCCCGCAACACCCCGACCTCAAAACGACGTCG 42634

QY 481 GCATCCGTTGGACAACAGCAACACGTCGTGTGCGGGTCTTCTGGACAACACCGCAACAG 540
DB 42633 GCATCCGTTGGACAACAGCAACACGTCGTGTGCGGGTCTTCTGGACAACACCGCAACAG 42574

QY 541 GGAGCACAGTCAAGCACTGTCAGCAACACCGGATCACCGCGCGCGCCCAAGCGTG 600
DB 42573 GGAGCACAGTCAAGCACTGTCAGCAACACCGGATCACCGCGCGCGCCCAAGCGTG 42514

QY 601 CCACAGTCTACCCCGCCCAACCAATATCCCGCAGGGGGTAAAGGACAGACCTTG 660
DB 42513 CCACAGTCTACCCCGCCCAACCAATATCCCGCAGGGGGTAAAGGACAGACCTTG 42454

QY 661 TCACACAGGGACAATCTGGAACGCTTCAAGAGTCTGAGGGTG 705
DB 42453 TCACACAGGGACAATCTGGAACGCTTCAAGAGTCTGAGGGTG 42409

```
RESULT 5
US-10-123-155-10/c
; Sequence 10, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-10

Query Match      5.4%; Score 38; DB 14; Length 594;
Best Local Similarity 8.0%; Pred. No. 0.057;
Matches 23; Conservative 126; Mismatches 140; Indels 0; Gaps 0;

QY 389 CACAGAGCGCGATAGTCTGTTTACACAGCCGCGCGTGGGTTTCGGGATCAT 448
DB 517 S.SDSYSYA.SYSYS.S.SWSSYSYSSDDY.CYCCYRYHCHSDSYSYY.CRCYYT 458
QY 449 CCCCAGAACACCCCCACCTCAACAGCGTCGCGCATCCGTTGGACACACAGCAGCTGG 508
DB 457 .SYSRYDCHYSCCSDYCYYSYSYSYSYSYSYSYSYSYSYSYSYSYSYSYSYS 398
QY 509 TGTGCGGGTCTTCTGGACACAAACCGCACGTCGCGCATCCGTTGGACACACAGCAGCTGC 568
DB 397 YSSSYSSAYSTSSSSSSSSYYTSTNYC.T.CC....T..MCAABCSTTTTTTTTT. 338
QY 569 CAACCGGATCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 628
DB 337 .HSCC.SA..A.M..YC.A.SYSYSYS.SSS.S.SYMR.HRA.SHYTTRS..S.MYCY.Y 278
QY 629 ATACCCCCCAGGGGGTAAAGGACAGACCTTGTTCACACAGCGGACAACTC 677
DB 277 M.Y..YY.YSYYSRKT.M....TWTDM.T.T..MHMY.KYB.HCHTKC 229

RESULT 6
US-10-146-731-10/c
; Sequence 10, Application US/10146731
; Publication No. US20030129692A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C168
; CURRENT APPLICATION NUMBER: P3330R1C168
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-146-731-10

Query Match      5.4%; Score 38; DB 15; Length 594;
Best Local Similarity 8.0%; Pred. No. 0.057;
Matches 23; Conservative 126; Mismatches 140; Indels 0; Gaps 0;

QY 389 CACAGAGCGCGATAGTCTGTTTACACAGCCGCGCGTGGGTTTCGGGATCAT 448
DB 517 S.SDSYSYA.SYSYS.S.SWSSYSYSSDDY.CYCCYRYHCHSDSYSYY.CRCYYT 458
QY 449 CCCCAGAACACCCCCACCTCAACAGCGTCGCGCATCCGTTGGACACACAGCAGCTGG 508
DB 457 .SYSRYDCHYSCCSDYCYYSYSYSYSYSYSYSYSYSYSYSYSYSYSYSYSYS 398
QY 509 TGTGCGGGTCTTCTGGACACAAACCGCACGTCGCGCATCCGTTGGACACACAGCAGCTGC 568
DB 397 YSSSYSSAYSTSSSSSSSSYYTSTNYC.T.CC....T..MCAABCSTTTTTTTTT. 338
QY 569 CAACCGGATCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 628
DB 337 .HSCC.SA..A.M..YC.A.SYSYSYS.SSS.S.SYMR.HRA.SHYTTRS..S.MYCY.Y 278
QY 629 ATACCCCCCAGGGGGTAAAGGACAGACCTTGTTCACACAGCGGACAACTC 677
DB 277 M.Y..YY.YSYYSRKT.M....TWTDM.T.T..MHMY.KYB.HCHTKC 229

RESULT 7
US-10-140-472-10/c
; Sequence 10, Application US/10140472
; Publication No. US2003013888A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C168
; CURRENT APPLICATION NUMBER: P3330R1C168
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-146-731-10
```

```

: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330RIC248
: CURRENT APPLICATION NUMBER: US/10/142,885
: CURRENT FILING DATE: 2002-05-10
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 10
: LENGTH: 594
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-10-142-885-10

Query Match          5.4%; Score 38; DB 16; Length 594;
Best Local Similarity 8.0%; Pred. No. 0.057;
Matches 23; Conservative 126; Mismatches 140; Indels 0; Gaps

Qy      389  CACAGAGCGCGATCAGTGTGCTTTACACAGCCGCGCGTGGCGTGTTCGGGATCAT
      .. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      517  S.SDSYSYA.SYSYS.S.SWSYSYSSSSDY.CYCCYRYHGSDSYSYSYTY.CRCCYTT
      .. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      449  CCGCGCAACACCCGCCACCTCAACACGACGTCCGCGATCCGTTGGACACACGACACAGTGGTGG
      .. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      457  .SYSRYDCHYSCCSDYCYYSYSRYYSYSYSWSYSYSYTDYCSYERCCCYYSYSSS
      .. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      509  TGTGCGGGTCTTCTGGACACAAACCCCAACAGGGAGACAGTCAAGACACTGTTCACGCCAA
      .. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      397  YSSSYSSAVSTSSSSSSSSSYTSTNYC.T.CC....T..MCABGCTTTTTTTTTT
      .. : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```



```
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C188
; CURRENT APPLICATION NUMBER: US/10/140,923
; PRIOR APPLICATION: 2002-05-07
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-923-10

Query Match          5.4%; Score 38; DB 17; Length 594;
Best Local Similarity 8.0%; Pred. No. 0.057;
Matches 23; Conservative 126; Mismatches 140; Indels 0; Gaps 0;

QY 389 CACAGAGCGCGCATCAGTCTGCTTTACAAACAGCCGCGCGTTCGGGATCAT 448
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 517 S.SDSYSA.SYSYS.S.SWSSYSYSSDDY.CYCCYRHCSDSYSYYY.CRCCYTT 458
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 449 CCCCACACACCCCCACCTCAACAGCAGTCGCGCATCGTTGGACACAGCAACACGTGG 508
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 457 .YSRYDCHYSCCSDYCYYSYRYSYSYSWSYSYTDYCSYRRCYYSYSS 398
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 509 TGTGGGGTCTTCTGGACAAACCGCAACAGGAGGACAGCTGTCACAGCAATC 568
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 397 YSSYSSAYSTSSSSSSSYTSTNYC.T.CC...T.MCAABGCTTTTTTTTTT 338
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 569 CAACCGGATCACCGCGCGCCCAAGCGTGCCACAGTCTACCCGCGCCCAACCCAAA 628
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 337 .HSCC.SA..A.M..YC.A.SYSYS.SSS.S.SYMR.HRA.SHYTTRS..S.MYCY.Y 278
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 629 ATACCCCCCAGGGGGTAAGGACAGACCTTGTCTACACACAGGACAATC 677
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-10-141-759-10/c
; Sequence 10, Application US/10141759
; Publication No. US20030207359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C197
; CURRENT APPLICATION NUMBER: US/10/141,759
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-759-10

Query Match          5.4%; Score 38; DB 17; Length 594;
Best Local Similarity 8.0%; Pred. No. 0.057;
Matches 23; Conservative 126; Mismatches 140; Indels 0; Gaps 0;

QY 389 CACAGAGCGCGCATCAGTCTGCTTTACAAACAGCCGCGCGTTCGGGATCAT 448
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 517 S.SDSYSA.SYSYS.S.SWSSYSYSSDDY.CYCCYRHCSDSYSYYY.CRCCYTT 458
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 449 CCCCACACACCCCCACCTCAACAGCAGTCGCGCATCGTTGGACACAGCAACACGTGG 508
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 457 .YSRYDCHYSCCSDYCYYSYRYSYSYSWSYSYTDYCSYRRCYYSYSS 398
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 509 TGTGGGGTCTTCTGGACAAACCGCAACAGGAGGACAGCTGTCACAGCAATC 568
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 397 YSSYSSAYSTSSSSSSSYTSTNYC.T.CC...T.MCAABGCTTTTTTTTTT 338
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 569 CAACCGGATCACCGCGCGCCCAAGCGTGCCACAGTCTACCCGCGCCCAACCCAAA 628
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 337 .HSCC.SA..A.M..YC.A.SYSYS.SSS.S.SYMR.HRA.SHYTTRS..S.MYCY.Y 278
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 629 ATACCCCCCAGGGGGTAAGGACAGACCTTGTCTACACAGGACAATC 677
Db      : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-10-141-756-10/c
; Sequence 10, Application US/10141756
; Publication No. US20030207359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C200
; CURRENT APPLICATION NUMBER: US/10/141,756
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
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QY 449 CCCCACACACCCACCTCAACAGCAGTCGGCATCCGTTGGCAACACAGCAACACGTCG 508
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 457 .SYSRYDCHYSCCSDYCYCYSYRYSYSYSSWSYSYTDYCSYRRCOCYYSYSS 398
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 509 TGTCCGGGTCTTCTGGACAACACCGCAACAGGAGCAGTCAAGCACTGTCAGCCAA 568
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 397 YSSSYSSSAYSTSSSSSSSYTYTNYC.T.CC...T.MCAABCSYTTTTTTTTT. 338
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 569 CAACCGGATCAGCCGCGCCGAGGCGTGCACAGTCTACCGCGCCCAACCCCAA 628
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 337 .HSCC.SA..A.M..YC.A.SYSYSY.SSS.S.SYMR.HRA.SHYTYS..S.MYCY.Y 278
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 629 ATACCCCCCAGGGGGTAAGGAGCAGACCTTGTCAACACAGGGAATC 677
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 M.Y..YY.YSYCSRKT....TWTDM.T.T..MHMY.KYB.HCHTKC 229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 15

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US-10-140-805-10/c
; Sequence 10, Application US/10140805
; Publication No. US20030207417A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C176
; CURRENT APPLICATION NUMBER: US/10/140,805
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-805-10
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Query Match          5.4%; Score 38; DB 17; Length 594;
Best Local Similarity 8.0%; Pred. No. 0.057;
Matches 23; Conservative 126; Mismatches 140; Indels 0; Gaps 0;

QY 389 CACAGAGCGCGATCAGTCTGCTTTACACAGCCGCGGTGGCGTTTTCGGGATCAT 448
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 517 S.SDSYSYA.SYSIS.S.SWSSYSYSSDDY.CYCCYRHCSDYSYSIY.CRCYIT 458
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 449 CCCCACACACCCACCTCAACAGCAGTCGGCATCCGTTGGCAACACAGCAACACGTCG 508
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 457 .SYSRYDCHYSCCSDYCYCYSYRYSYSYSSWSYSYTDYCSYRRCOCYYSYSS 398
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 509 TGTCCGGGTCTTCTGGACAACACCGCAACAGGAGCAGTCAAGCACTGTCAGCCAA 568
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 397 YSSSYSSSAYSTSSSSSSSYTYTNYC.T.CC...T.MCAABCSYTTTTTTTTT. 338
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 569 CAACCGGATCAGCCGCGCCGAGGCGTGCACAGTCTACCGCGCCCAACCCCAA 628
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 337 .HSCC.SA..A.M..YC.A.SYSYSY.SSS.S.SYMR.HRA.SHYTYS..S.MYCY.Y 278
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 629 ATACCCCCCAGGGGGTAAGGAGCAGACCTTGTCAACACAGGGAATC 677
```

```
Db 277 M.Y..YY.YSYCSRKT....TWTDM.T.T..MHMY.KYB.HCHTKC 229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: September 26, 2005, 01:30:26
Job time : 679 secs
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